## Schreiber, David

From:

Fredman, Jeffrey

Sent:

Wednesday, January 19, 2005 10:34 AM

To: Cc: Schreiber, David

Subject:

Chunduru, Suryaprahbha FW: ref to rush sequence search for case # 09/603,665

David,

I Approve the Rush.

0

I am not exactly sure what Prabha means to search, but perhaps she means the 20-30 nucleotides overlapping each of the listed positions.

#### Jeff Fredman

----Original Message-----

From:

Chunduru, Suryaprahbha

Sent:

Wednesday, January 19, 2005 9:41 AM

To:

Fredman, Jeffrey

Subject:

ref to rush sequence search for case # 09/603,665

Hi Jeff,

I request you to approve a rush sequence search for the above amended case. Oligomer search for sequences comprising positions 1694, 1854, 1967, 2017, 2050 of SEQ ID NO. 5. I resquest David Schreiber to perform the search.

thanks Suryaprabha Chunduru AU 1637, Room No. 2C29, Mail box 2C18 tel. # 272-0783.

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Access	DB#		

## SEARCH REQUEST FORM

### Scientific and Technical Information Center

Requester's Full Name:		Examiner # :	
Art Unit: Phone I	Number 30	Serial Number:	DIDED DICK FALL
Mail Box and Bldg/Room Locatio	n: R	Results Format Preferred (circ	le): PAPER DISK E-MAI
If more than one search is subn	nitted, please prior	ritize searches in order of ********	need. *********
Please provide a detailed statement of the Include the elected species or structures, utility of the invention. Define any terms known. Please attach a copy of the cover	keywords, synonyms, a s that may have a specia	cronyms, and registry numbers, and meaning. Give examples or rele	nd combine with the concept or
Title of Invention:			
inventors (please provide full names):			
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*For Sequence Searches Only* Please inclu appropriate serial number.	ide all pertinent informati	ion (parent, child, divisional, or issue	ed patent numbers) along with the
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# STIC Search Report Biotech-Chem Library

# STIC Database Tracking Number: 144006

TO: Suryaprabha Chunduru Location: REM/2C29/2C18

Art Unit: 1637

Wednesday, February 02, 2005

Case Serial Number: 09/603665

From: David Schreiber

**Location: Biotech-Chem Library** 

Remsen E01A61 Phone: 272-2526

david.schreiber@uspto.gov

Search Notes	



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   RESULT 1
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97US-0042611P.
97US-0042985P.
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AAO10626
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ABG37283
                                                                                                                                                                                                                                                                                                                                                                                              breast cancer; risk; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM55323
                                                                                                                                                          3123, BE2, BB14, BB31 or BE445 - which as binding proteins are useful to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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The present invention describes primer sets for synthesising 5602 full-CC length cDNAs defined in the specification. Where a primer set comprises: CC (a) an oligo-dT primer and an oligonucleotide complementary to the CC complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC omplementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the CC specification. The primer sets can be used in antisense therapy and in CC gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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detect BARD1, B123, BE2,
antibody can be used to i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:11159.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; SEQ ID NO 11159; 2537pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HELIX RES
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nilarity 100.
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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T, Wakamatsu
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, BE14, BE31 or BE445, a specific anti-BARD1
identify a patient having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; antisense therapy; gene therapy
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A, Nagai K,
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C, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 349 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang Y
Ghosh
Ma Y,
                                                  tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                             New polynucleotides, useful for expressing recombinant proteins analysis, characterization or therapeutic use, or as markers fo in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                      The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or
                                                                                                                                                                                                                                                                                   Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2002;
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12-APR-2002;
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14-MAR-2002;
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11-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel protein (useful for identifying genetic disorders) #167
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DB; ADE07101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC.
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                                                                                                                                                                                                                                                                                   SEQ
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Xue AJ, Wehrman T, Weng G, Zhou
ng D, Chen R, Xu C, Boyle BJ;
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2002US-0372615P.
2002US-00128558.
2002US-0376045P.
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2001US-0339453P.
2002US-0365091P.
2002US-0365384P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002WO-US039555
                                                                                                                                                                                                                                                                             ID NO 1078; 1177pp; English.
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ou P,
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Perfect score:
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 Pred. No.
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Abu42163 Protein e
Abm89250 Photorhab
Adf06196 Bacterial
Abu40177 Protein e
Abo63337 Klebsiell
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Ade08012 Novel pro
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Abb11340	Aao02776	Aam89692	Adk36989	Aao06065	Aao11546	Aau79243	Abo56259	Aao09971	Aao03775	Aa008667	Aam06778	Aam91234	Ade46243	Abg21112	Aam96713	Aau22275	Aau18927	Aag00262	Aao04449
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ALIGNMENTS

### ARESULT 1 ARMYS 4099 ID ARMYS 4099 ID ARMYS 4099 AC ARMYS 2000 20-SEP-1996; 03-APR-1997; 04-APR-1997; W09812327-A2. BARD1; ring protein; BRCA1; breast cancer; risk; diagnosis. AAW54099; 19-SEP-1997; 26-MAR-1998. Homo sapiens Homo sapiens BAP28 sequence 28-SEP-1998 AAW54099 standard; protein; (first 96US-0025296P. 97US-0042611P. 97US-0042985P. 97WO-US016842 entry) ξ

The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, B123, BE2, BE14, BB31 or BE445, or a composition for the detection of a BARD1, B123, BE2, BE14, BB31 or BE445 nucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BRCA1, useful to identify a patient having, or at risk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the biological activity of the BRCA1-BARD1,

DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.

Disclosure; Page 287-288; 348pp; English.

WPI; 1998-230317/20. N-PSDB; AAV24135.

Bowcock AM, Baer R;

(TEXA ) UNIV TEXAS SYSTEM.



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The present invention describes primer sets for synthesising 5602 full-
clength cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
cnucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
cof an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
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complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a sequence, where the
complementary to a
complementary strand of a polynucleotide which comprises and the combination of
complementary strand of a polynucleotide which comprises and the combination of
complementary strand of sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
complementary strand of the abnormality of the proteins encoded by
complementary strand of the primers allow obtaining of the full-length
complementary to the primers allow obtaining of the full-length
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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antibody can be used
developing cancer
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                                                                                                                                                                                                                                                                                                                                                                                       diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                sets for synthesizing polynucleotides, particularly the 5602 full-
cDNAs defined in the specification, and for the detection and/or
sis of the abnormality of the proteins encoded by the full-length
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Sugiyama
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ilarity 100.0%;
Conservative (
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2000JP-00183767.
2000JP-00241899.
                                                                                                                                                                                                                                                                                                                         ID NO 11159; 2537pp + Sequence Listing; English
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99JP-00300253.
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 or BE445 complex. The antibodies can be used to BE2, BE14, BE31 or BE445, a specific anti-BARD1 d to identify a patient having or at risk of
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Pred. No. 8.6
0; Mismatches
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A, Nagai K,
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, Otsuki T;
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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.

Sequence 1149

New polynucleotides, useful for expressing recombinant proteins analysis, characterization or therapeutic use, or as markers for which the corresponding protein is preferentially expressed.

for tissues

Claim 20; SEQ ID NO 1078; 1177pp; English.

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RESULT 3
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AND ADEGRACI
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Best Local
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365991P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-037255P.
22-APR-2002; 2002US-0376045P.
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Ma Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
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Xue AJ, Wehrman T, We
ang D, Chen R, Xu C, B
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Perfect score:
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210.782 Million cell updates/sec
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20-SEP-1996;
03-APR-1997;
04-APR-1997;
                                                                                                                          19-SEP-1997;
                                                                                                                                                                     Homo sapiens BAP28 sequence
                                                                                         Bowcock
                                                                                                 (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                   26-MAR-1998.
                                                                                                                                           W09812327-A2
                                                                                                                                                    Homo sapiens.
                                                                                                                                                            BARD1; ring protein; BRCA1; breast cancer; risk; diagnosis.
                                                                                         AM,
                                                                                                         96US-0025296P.
97US-0042611P.
97US-0042985P.
                                                                                                                          97WO-US016842.
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DNA sequence encoding BARD1, B123, BE2, BE14, BE31 breast cancer antigen, BRCA1, binding proteins are patient having or at risk of developing cancer. 1123, BE2, BE14, BE31 or BB445 - which as binding proteins are useful to identify

WPI; 1998-230317/20. N-PSDB; AAV24135.

Disclosure; Page 287-288; 348pp; English.

The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BRCA1, useful to identify a patient having, or at risk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the biological activity of the mochi-mach



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         The present invention describes primer sets for synthesising 5602 full-CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 cc mucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the CC omplementary strand of a polynucleotide which comprises a 5'-end cc gequence and an oligonucleotide comprising a sequence complementary to a composition of cc sequence comprises a 1'-end sequence complementary to a cc polynucleotide which comprises a 1'-end sequence, where the cc pecification. The primers are useful for matisense therapy and in cc gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the comprise and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also the the fill-length cDNAs. The primers are also the condition of the fill-length cDNAs. The primers also the condition of the fill-length cDNAs. The primers also the condition of the fill-length cDNAs. The primers also the condition of the fill-length cDNAs. The primers also the condition of the condition of the fill-length cDNAs. The primers also the condition of the condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
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27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 ful length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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, Sugiyama
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                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 11159; 2537pp + Sequence Listing; English
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T, Wakamatsu
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C, Otsuki
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Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac F Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

RT,

New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tin which the corresponding protein is preferentially expressed.

tissues

N-PSDB; ADE07101.

2003-569235/53.

Claim 20; SEQ ID NO 1078; 1177pp; English.

The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein

full-length cDNAs. The primers allow

obtaining of the full-length

Sequence 1149

invention.

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RESULT 3
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11-DEC-2001; 2001US-0339453P.
11-MAR-2002; 2002US-0355091P.
14-MAR-2002; 2002US-0355384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-03725615P.
22-APR-2002; 2002US-0376045P.
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ABO55613 ABU40981 ABP07304 AAM92148 AAM1530 ABB34537 AAM28020 ABB29363 ABB19946 AAM67720

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The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BRCA1, useful to identify a patient having, or at risk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the biological activity of the BRCA1-BARD1,

Peptide Protein

AAM74002 AAM61279 ABG55759 ABG43897 ABU60930

Aam61279 Aam74002 Abb40457

Aam34177

Peptide Peptide

DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.

Disclosure; Page 287-288; 348pp; English.

ABB40457 AAM34177

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WPI; 1998-230317/ N-PSDB; AAV24135.	Bowcock AM,	(TEXA )	20-SEP-1996; 03-APR-1997; 04-APR-1997;	19-SEP-1997	26-MAR-1998	W09812327-A2	Homo sa	BARD1;	Homo sa	28-SEP-1998	AAW54099;	RESULT 1 AAW54099 ID AAW54099 XX		45	44.	2 2	41	40	9 6	37	36		3 L	32	31	30	29	9 .	3 6	,
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				•				breast cancer;				515 AA.	ALIGNMENTS	AAM80897	15554010 1A877507	ADM19866	DK36505	AAY07240	AAY07241	AA010626	AB42068	1BG13882	AAUI /456	AAG01570	DM26908	A007992	DK34692	ABG37283	AAM55323	7 3
							,	; risk; diagnosis.						Human	Aar77507 Human neu		-	_	Aay07241 Fragment			Nove1	Aabi 9971 Human STA	Human	Hypert			Human	Abraessa Human liv	Himan

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The present invention describes primer sets for synthesising 5602 full-
calculation of the specification. Where a primer set comprises:
calculation of the specification of the set comprises:
calculation of primer and an oligonucleotide complementary to the
calculation sequences defined in the specification, where the
calculation of a polynucleotide sequence complementary to the
calculation of a polynucleotide sequence complementary to the
calculation of a polynucleotide which comprises a 5'-end
calculation of a polynucleotide which comprises a 5'-end
calculation of a polynucleotide comprises a 5'-end
calculation of a polynucleotide comprises a 5'-end
calculation of a polynucleotide comprises a 5'-end
calculation of sequence is sequence, where the
calculation of sequence is sequence is selected from those defined in the
calculation. The primer sets can be used in antisense therapy and in
calculation of the sprimers are useful for synthesising polynucleotides,
calculation of the sprimers are useful for synthesising polynucleotides,
calculation and/or diagnosis of the abnormality of the proteins encoded by
chastinian and/or management and allow obtaining the proteins encoded by
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Matches 41
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T,
Ishii
                                                                                                                                                                                                                                                                          Claim 8;
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; 2000JP-00118776.
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T, Wakamatsu
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Matches
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                   proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents
                                                                                                                                                                                                                                Ghosh
Ma Y,
                                                                                                                                                New polynucleotides, useful for expressing recombinant proteins analysis, characterization or therapeutic use, or as markers for in which the corresponding protein is preferentially expressed.
                                                                                                                            Claim
                                                                                                                                                                                                                                                       Tang
                                                                                                                                                                                                                                                                                                              12-APR-2002;
22-APR-2002;
                                                                                                                                                                                                                                                                                                                                              14-MAR-2002;
14-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                    10-DEC-2001;
11-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB52446 to AAB589: represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                   24-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003054152-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
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                                                                                                                                                                                                                                                                                                                                     12-APR-2002;
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ц,
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DB; ADE07101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                              F, Asundi V, Goodri
M, Xue AJ, Wehrman '
Wang D, Chen R, Xu
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                                                                                                                           SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marker;
                                                                                                                                                                                                                                                                                                7 2001US-0339739P.

7 2001US-0339453P.

7 2002US-0355091P.

7 2002US-0355384P.

7 2002US-0372381P.

7 2002US-0372381P.

7 2002US-0372615P.

7 2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel protein; tissue marker; molecular weight marker; marker; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                       2002WO-US039555
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                                                                                                                          1078; 1177pp; English.
                                                                                                                                                                                                                              Goodrich RW, Ren F, Zhang
ehrman T, Weng G, Zhou P,
R, Xu C, Boyle BJ;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Pred. No.
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1e-13;
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anac RT,
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Query Match Best Local S Matches 20

Similarity

48.8%; Score 20; 100.0%; Pred. No.

20;

Conservative

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Mismatches

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3e-13;

DB 7; Length 1149; 0;

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AABBSULT 4
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     Query Match 48.8%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 5.7 Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                  sequences and regulatory region located at the 3 and 5 ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polymuclectides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallatic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first CDNA sequence of the BAP28 gene consisting of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3^{\prime} and 5^{\prime} ends of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barry C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999; 99US-0141323P.
18-JAN-2000; 2000US-0176880P.
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                                                                                                                          Sequence 2144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 297-304; 349pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
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/label= Gly or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1967
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DB 4; L., 5.3e-13; 0;
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                                                              Length 2144;
              Indels
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RESULT 6 ABO62754 ID ABO6

ABO62754 standard; protein; 650

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RESULT 5
ABM73641
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                                                      Matches
                                                                                Query Match
                                                                                                                                                                 barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                             Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2001; 2001JP-00387059
20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299
20-DEC-2001; 2001JP-00403300
27-SEP-2002; 2002JP-00327515
                                                                                                                                          at ftp.wipo.int/pub/published-pct-sequences. (Updated
standardise OS field)
                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare; var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA clone originating in barley containing SNP sequence #51.
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17-OCT-2003
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                                                                                                                                                                                                                                                                                                    The present invention relates to oligonucleotide clones originating
                                                                                                                                                                                                                                                                                                                                                         characteristics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis
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                                                                    Local
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 45
                          26 PLVDQLE 32
                                                     7; Conserv
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PLVDQLE
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                                                        Conservative
                                                                                                                                                                                                                                                                                                                             SEQ ID XX; 284pp; Japanese
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(first entry)
 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kohara
                                                                       100.0%;
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                                                                       Score 7;
Pred. No.
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                                                      Mismatches
                                                              DB
11;
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Best Local S
Matches 7
                                                                                                  Rice; polyadenylated RNA-binding protein; transgenic plant; herbicide; eukaryotic translation initiation factor-4 (eIF-4) gamma; genetic mapping; physical mapping.
         02-JUL-1999;
                                 25-SEP-2001.
                                                       US6294658-B1
                                                                              Oryza sativa
                                                                                                                                                  Rice poly
                                                                                                                                                                           28-JAN-2002
                                                                                                                                                                                                 AAE13001;
                                                                                                                                                                                                                      AAE13001 standard;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 650 AA;
                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                (A) binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae polypeptide seqid 9271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                         17.1%; Score 7; DB larity 100.0%; Pred. No. 55
Conservative 0; Mismatches
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         99US-00347833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO
                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9271; 932pp; English.
                                                                                                                                                                                                                      655
                                                                                                                                              from clone rsr9n.pk005.117.
                                                                                                                                                                                                                                                                                                                                    DB 7;
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                                                                                                                                                                                                                                                                                                                                                Length 650;
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31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000;

; 2000US-0179065P. ; 2000US-0180628P. ; 2000US-0184664P. ; 2000US-0186350P. ; 2000US-0189874P. ; 2000US-0190076P.

17-JAN-2001; 16-AUG-2001 WO200159063-A2

2001WO-US001334.

Homo

sapiens.

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RESULT 8
ABB15816
ID ABB1
XX ABB1
AC ABB1
XX ABB1
XX ABB1
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Immu
XW anti
XW Immu
XW ATI

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergac; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyadenylated RNA-binding protein or eukaryotic translation initiation factor-4 (eIF-4) gamma. The nucleic acid fragments may be used in PCR protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA, to create transgenic plants in which the new polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. The nucleic acids may also be used as probes for genetic or physical mapping the genes that they are part of and as makers for traits linked to those genes. The polypeptides may be used to produce antibodies and as targets to facilitate design and/or identification of inhibitors of those enzymes that can be used as herbicides. The present sequence is rice poly (A) binding protein from clone rsr9n.pk005.117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human nervous system related polypeptide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9;
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20-OCT-2000;
20-NOV-2000;
20-NO
                                                                          Nucleic acids encoding useful for preventing, and metastases.
                                                                                                                                       WPI; 2001-541565/60.
N-PSDB; ABA12142.
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                                                                                                                                                                                       SC,
                                                                                                                                                                                                                      SCI
                                                                                          3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system cancers
                                                                                                                                                                                       Ruben
                                                                                                                                                                                       SM.
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating

Claim 11; SEQ ID NO 4473; 1701pp + Sequence Listing; English.

ק ארים קרים רו ביו קרים רו ביו קרים לו היו לי אים לו אים לו היו לו הי

18 APR-2000
17-JUN-2000
28-JUN-2000
28-JUN-2000
29-JUN-2000
11-JUL-2000
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2000US-0198123P 2000US-0209467P 2000US-0216486P 2000US-021647P 2000US-021647P 2000US-021647P 2000US-021647P 2000US-021647P 2000US-021648P 2000US-0225451P 2000US-0225214P 2000US-0225266P 2000US-0225266P 2000US-0225275P 2000US-0225266P 2000US-0225276P 2000US-0225276P 2000US-0225279P 2000US-0225279P 2000US-0225279P 2000US-0225279P 2000US-0225279P 2000US-0225279P 2000US-022528P 2000US-02252934P 2000US-0231413P 2000US-0231413P 2000US-0231413P 2000US-0231413P 2000US-0231413P 2000US-0231413P 2000US-0231413P 2000US-0231414P 2000US-023349P 2000US-023349P 2000US-023349P 2000US-023349P 2000US-023349B 2000US-023349B 2000US-023349B 2000US-023349B 2000US-023349B 2000US-0233935P 2000US-0233935P 2000US-0233935P

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RESULT 9
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Best Local S
Matches 6
    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in all of the printed specification, but was obtained in all of the printed specification, but was obtained in all of the printed specification, but was obtained in all of the printed specification, but was obtained in all of the printed specification, but was obtained in all of the printed specification, but was obtained acid probe that the probability of the printed specification, but was obtained acid probe that the probability of the printed specification, but was obtained acid probe the probability of t
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                                                                                                                                                                                       Claim 27;
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2000US-0207456P.
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but was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid probe
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                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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RESULT 11 AAM74002

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AAM34177
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                                 Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local
                                                                                                                                                                                                                                                                03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                      Sequence 36
                                                                                     The present invention relates to single exon nucleic acid probes (see AAI31315-AAI57546). The present sequence is a peptide encoded be such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples defrom human placenta. The probes are useful for antenatal diagnosis human genetic disorders
                                                                                                                                                                                                                    Penn
                                                                                                                                                      Claim
                                                                                                                                                                                  Human
                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312P
26-MAY-2000; 2000US-0207456P
30-JUN-2000; 2000US-00608408
                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                        04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       genetic
                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #8214 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM34177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM34177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                       expression in
                                                                                                                                                                                                  2001-488897/53.
                                                                                                                                                                                                                    SG
                36
                                                                                                                                                       27;
                                                                                                                                                                              genome-derived single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 GGEEKF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                       disorder.
                GGEEKF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGEEKF
                                                                                                                                                       SEQ ID
                                                                     ₽¥,
                                 Conservative
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2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                        2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                    NO 34446;
                                                                                                                                                                                                                   봈
                                                                                                                                                                    human placenta
                                                                                                                                                                                                                                                                                                                                                                                                              human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                          100.0%;
                                                   14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.6%;
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                                k; Score 6; DB 4
k; Pred. No. 50;
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                   Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                              measuring placental gene expression.
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                                                  Length 36;
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RESULT 12
AAM61279
ID AAM61
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AC AAM61
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                              Human brain expressed single exon probe encoded protein SEQ ID NO: 33384.
                                                                                                                                                                                                                                                                                                                              Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 34308; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
             WO200157275-A2
                                                            Alzheimer's
                                                                                                                       05-NOV-2001
                                                                                                                                                                      AAM61279 standard; protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human bone marrow expressed probe encoded protein SEQ ID NO:
                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM74002 standard; protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                                        36 GGEEKF 41
                                                                       brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                 GGEEKF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma.
                                                           disease;
                                                         expressed exon; gene expression analysis; probe; microarray; disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312P.
2000US-0207456P.
                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                          14.6%; but
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone
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                                                                                                                                                                                                                                                                                          Score; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                marrow.
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                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                          DB 4;
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RESULT 13
ABG55759
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Best Local (
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                       ABG55759 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one othe probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
                                                                                                             30-JAN-2001; 2001WO-US000664
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                             Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                          Human liver peptide, SEQ ID No 34407.
                                                                                                                                                                                                                                                25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
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                                                                                                                                 09-AUG-2001.
                                                                                                                                                      WO200157273-A2
                                                                                                                                                                                            hypercholesterolaemia; coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4;
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          (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                              36 GCEEKF 41
                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
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                                                                                                                                                                                                                                                                                                                                           GGEEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                      ; 2000US-0180312P.
2000US-0207456P.
2000US-00608408.
; 2000US-00632366
; 2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes
                                                                                                                                                                                                                                              (first entry)
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2000US-0207456P.
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                               2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                           14.6%;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 6;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Listing;
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50;
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 36;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 14
ABG43897
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Best Local Similarity
Marches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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26-MAY-2000;
                                                                                         03-AUG-2000;
                                                                                                        30-JUN-2000;
                                                                                                                                                                                                    15-NOV-2001.
                                                                                                                                                                                                                                  WO200186003-A2
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                      Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                    Human, single exon probe; asthma; lung cancer; COPD; IID; chronic obstructive pulmonary disease; interstitial lung disease; interstitial lung disease; interstitial filling disease; interstitial pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG43897 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human niver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                  30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                               membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGEEKF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 34407; 658pp; English.
                                                                                      ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                          2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded by genome-derived single exon
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o. 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               probe SEQ ID 33562
                                                                                                                                                                                                                                                                                                                                                                                                   disease;
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ABUG0930
ID ABUG0930
XX ABUG0
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XX ABUG0
XX LUNG
DT 08-MA
XX LUNG
DE LUNG
XX HUMAN
KW HUMAN
KW non-c
XX

08-MAY-2003 ABU60930;

(first entry)

Lung specific protein (LSP)

#33.

ABU60930 standard; protein; 48 AA.

Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal.

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Query Match
Best Local Similarity
Matches 6; Conser

14.6%; Score 6; DB ilarity 100.0%; Pred. No. 50 Conservative 0; Mismatches

DB 50; 5;

Length 36;

0

0

Gaps

36

GGEEKF 41

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mucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12397 open reading frames derived from the 12614 probes. Also included are a microarray comprising the movel set of probes derived from human lung, comprising the movel set of probes collection of detectably labeled nucleic acids derived from human lung, comprising (a) contracting the array with a collection of detectably labeled nucleic acids derived from human lung measuring gene expression in a sample company, and (b) measuring the label detectably bound to each probe of the carray; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eakaryotic; and (b) detecting specific bybridisation of detectably labeled nucleic acids from eukaryote lung mkNA, to a single exon probe, and the above mentioned microarray; assigning exons to a single exon probe, and the above mentioned microarray; assigning exons to a single exon probe, and the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several cissues and/or cell types using hybridisation to a single exon comprising exons and/or cell types indicates that the exons should be assigned to a single gene, particularly using human continuity sequences, mentioned in the specification, or encoded by the exons should be assigned to a single gene, particularly using human continuity derived mRNA and for the study of lung disease such as asthma, lung disease (ILD), familial idiopathic pulmonary haemosiderosis, neurofibromatosis, pulmonary hypertensis, pulmonary protesing, pulmonary sequences, particularly using human contents. Pulmonary hypertensis, pulmonary sequences, particularly decomprises, pulmonary hypertensis, pulmonary cont
Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 33562; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used
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                                                                     Query Match 14.6%; Score 6; DB 5; Best Local Similarity 100.0%; Pred. No. 65; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                     The invention describes an isolated human nucleic acid (I) encoding any of 120 10-153 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This is the amino acid sequence of a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                           Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 328; 389pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-713376/77.
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42 PLVDQL 47
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	Human	Human	Human	Novel	Human	Novel	Human	Human	Novel	Human	Human									

ALIGNMENTS

### RESULT 1 AAW54099 20-SEP-1996; 03-APR-1997; 04-APR-1997; BARD1; ring AAW54099; Bowcock AM, 19-SEP-1997; Homo sapiens. Homo sapiens BAP28 sequence 28-SEP-1998 AAW54099 standard; protein; WO9812327-A2. (TEXA ) UNIV 26-MAR-1998. protein; BRCA1; breast cancer; risk; diagnosis. Baer R; TEXAS SYSTEM. (first entry) 96US-0025296P. 97US-0042611P. 97US-0042985P. 97WO-US016842 515 B

Disclosure; Page 287-288; 348pp; English.

DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.

N-PSDB; AAV24135. WPI; 1998-230317/20.

agonist or antagonist that alters the binding or μακύι, μιζί, μεζί, με BE31 or BE445 to BRCA1 or the biological activity of the BRCA1-BARD1,

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The present invention describes primer sets for synthesising 5602 full—CC (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 CC complementary strand of a polynucleotide which comprises one of the 5602 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC complementary strand of a polynucleotide which comprises at 5 end CC sequence and an oligonucleotide comprising a sequence complementary to the CC sequence and an oligonucleotide comprising a sequence complementary to a combination CC complementary strand of a polynucleotide which comprises a 5 end sequence, where the CC polynucleotide which comprises a 3 end sequence, where the CC polynucleotide which comprises a 3 end sequence, where the CC specification. The primers set can be used in antisense therapy and in the CC gene therapy. The primers set useful for synthesising polynucleotides, can be used in antisense therapy and in CC gene therapy full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers also useful for the full-length cDNAs. The primers also useful for the complementary com
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Matches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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02-MAY-2000;
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27-AUG-1999;
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detect BARD1, B123, BE
antibody can be used t
developing cancer
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa
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A, Nagai K,
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C, Otsuki
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RESULT 3
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-0376045P.
                     The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                  Ghosh
Ma Y,
                                                                                                                                            New polynucleotides, useful for expanalysis, characterization or there in which the corresponding protein
                                                                                                                        Claim 20; SEQ ID NO 1078; 1177pp;
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                                                                                                                                                                                                                                                                                  (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention
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                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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Xue AJ, Wehrman 1
ng D, Chen R, Xu
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Wehrman T, Wen
a R, Xu C, Bc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder.
                                                                                                                                           for expressing recombinant proteins or therapeutic use, or as markers for protein is preferentially expressed.
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                                                                                                                                                                                                                                RW, Ren F, Zh
Weng G, Zhou
Boyle BJ;
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Pred. No.
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8.5e-13;
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ou P,
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Drmanac R
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Similarity

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Matches 20
     Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                      The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polymucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first cDNA sequence of the BAP28 gene consisting of the exons 1 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1999; 99US-0141323P.
18-JAN-2000; 2000US-0176880P.
                                                                                                         Sequence 2144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 297-304; 349pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barry C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-2000; 2000WO-IB001183.
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     48.8%; Score 20; DB ilarity 100.0%; Pred. No. 3.0 Conservative 0; Mismatches
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                                                    Length 2144;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klebsiella pneumoniae.
                                                   Antisense; prokaryotic essential gene; cell proliferation;
                                                                                                         Protein
                                                                                                                                                               19-JUN-2003
                                                                                                                                                                                                                     ABU42163;
                                                                                                                                                                                                                                                                     ABU42163 standard; protein; 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
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                                                                                                         encoded by
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.5%; Score 8; DB larity 100.0%; Pred. No. 4. Conservative 0; Mismatches
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                                                                                                                                                            (first entry)
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                                                                                                         Prokaryotic essential gene #27690
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                                                     drug design.
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Pseudomonas syringae

WO200277183-A2

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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits promiter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated cc nucleic acid; (4) an antibody capable of specifically binding cantisense nucleic acid; (4) an antibody capable of specifically binding polypeptide; (5) producing the polypeptide; (6) inhibited by the cc proliferation or the activity of a gene in an operor required for proliferation, or that this influences the activity of identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway considered for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation, or that inhibits proliferation or the biological corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the extent strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation of compound that inhibits of compound that inhibits of compound that inhibits in which the extent strains; or constitution to isolate candidate molecules for rational constituted for proliferation in cells other than S. aureus, S. typhimurium, C. auteur for proliferation in cells other than S. aureus, S. typhimurium, constituted for proliferation in cells other than S. aureus, S. typhimurium, constituted for proliferation in cells other than S. aureus, S. typhimurium, constituted for proliferation to isolate candidate molecules for rational constitution of the carget prokary the constitution of the printed spe
                                                                         Query Match
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Matches 8
                                                                                                                                                   Sequence
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25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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67
                                  34 LTAFFLEA
                                                                         Similarity
8; Conserv
LTAFFLEA 74
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Trawick JD,
                                                                     ilarity 100.0%; I Conservative 0;
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                 19.5%; Score 8; DB 6;
100.0%; Pred. No. 4.5;
tive 0; Mismatches
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Carr GJ,
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Forsyth
                                                                                                        Length 443;
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Xu HH;
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ABM69250 standard; protein; 446

RESULT 8 ADF06196

ADF06196 standard; protein;

457

ADF06196

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103

LTAFFLEA 110

34 LTAFFLEA 41 Similarity 8; Conserv

Matches

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The invention relates to the isolation of genes and their encoded CC proteins from Photorhabdus luminescens. The isolated sequences are CC sources of probes and primers for detecting the genome of P. luminescens CC and related species; to study polymorphisms; for gene analysis and for CC detection/amplification of the genes. Antibodies (Ab) raised against the polymprophisms proteins, Ab and cells that CC carry a gene-containing vector are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that CC modulate, regulate, induce or inhibit expression of the genes in plants, response or microorganisms other than P. luminescens and are able to alter compounds that the compounds or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and cells that CC genes, proteins, vectors containing the genes and Ab are also useful therefore, proteins, vectors containing the genes and are also useful thereses, proteins, vectors containing the genes and are also useful thereses, proteins, vectors containing the genes and have also useful that are sensitive to P. luminescens encoded toxins or antibiotics) and as CC biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                            Query Match
Best Local
                                                                                      Sequence 446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 2347; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-148459/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchrieser C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2001; 2001FR-00001659
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            whooping cough.
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                       19.5%;
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b; Score 8; DB 6
b; Pred. No. 4.6
0; Mismatches
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                     DB 6;
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                                         Length 446
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new Proteus mirabilis polypeptides and polynucleotides. The invention also relates to antibodies against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-895291/82.
N-PSDB; ADF02024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 457 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biocontrol agents for plants.
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                                                               WO200277183-A2
                                                                                                                       Pseudomonas putida
                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #25704.
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8; Conservative
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100.0%; Pred. No.
174 0; Mismatches
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03-OCT-2002

29-JUL-2004

(first entry)

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RESULT 10
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SXR
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Wall D,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                       K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published not format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
                                         ABO63337;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                    ABO63337 standard; protein; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 68101; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                    92 LTAFFLEA 99
                                                                                                                                                                                                                                               34 LTAFFLEA 41
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA44047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio
Trawick
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ģς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                           19.5%;
                                                                                                                                                                                                                                                                                             Score 8; DB 6; Pred. No. 4.7
0; Mismatches
                                                                                                                                                                                                                                                                                               0,
                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                     DB 6;
5. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                           Length 467;
                                                                                                                                                                                                                                                                                               Indels
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Xu HH;
                                                                                                                                                                                                                                                                                               0,
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RESULT 11
ADF04247
ID ADF04
XX ADF04
XX ADF04
XX ADF04
XX Bacte
XX Prote
XX Prote
XX Immur
XX Immur
XX Immur
XX Prote
PN US660
YX U5660
YX 05-AE
YX 09-AE
YX 09-AE
PA (GENC
XX Bretc
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
  Breton GL
                                                 09-APR-1999;
                                                                          05-APR-2000;
                                                                                                   12-AUG-2003.
                                                                                                                           US6605709-B1.
                                                                                                                                                     Proteus mirabilis
                                                                                                                                                                             immunostimulant.
                                                                                                                                                                                   Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                 Bacterial polypeptide #360.
                                                                                                                                                                                                                                                                   ADF04247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                          (GENO-) GENOME
                                                                                                                                                                                                                                          12-FEB-2004
                                                                                                                                                                                                                                                                                        ADF04247 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 9854; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACH96888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breton GL, Osborne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae polypeptide seqid 9854,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                        111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-895346/82
                                                                                                                                                                                                                                                                                                                                                                               34 LTAFFLEA 41
                                                                                                                                                                                                                                                                                                                                                        LTAFFLEA 118
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                         2000US-00543681.
                                                                                                                                                                                                                                         (first entry)
                         THERAPEUTICS CORP.
                                                 99US-0128706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0117747P.
                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 7; Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription regulatory element; antibacterial; Vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 473;
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RESULT 12
ABO71657
ID ABO71
XX ABO71
XX ABO71
XX ABO71
XX Bacte
XX
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Best Local
                                                                                                                        Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new Proteus mirabilis polypeptides and polypucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                         Disclosure; SEQ ID NO 20403; 455pp; English
                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                      Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO71657 standard; protein; 492
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa polypeptide #3832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 4532; 870pp; English
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                                                                                                                                                                                                                                                       2003-615309/58.
DB; ABD05228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 LTAFFLEA 146
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                Nolling
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98US-0094190P
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                                                                                                                                                                                                                                                                                                                                Deloughery
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                   Bush
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis

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Best Loc
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Best Local
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                          Novel AtMID1B gene derived from Arabidopsis thaliana encoding extension-activated calcium permeable channel, useful for maintaining gravity tropism in plant.
                                                                                                                                                                                                                                                                                                               WPI; 2003-819302/77.
N-PSDB; ADG36881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MID1B; extension-activated calcium permeable channel; plant; gravity; tropism; gravity sensor; photosynthesis.
                                                                                                                     This invention describes a novel gene (AtMDIB) encoding an extension-
activated calcium (Ca2+) permeable and of higher plant, useful for
controlling gravity tropism in plants. The gene is useful as gravity
sensor in plant. Transgenic plants containing the gene have improved
                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2001; 2001JP-00385513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 2001JP-00385513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2003180367-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. thaliana MID1B protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2004
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                                                                      Sequence
                                                                                                        photosynthetic
                                                                                                                                                                                                           Claim 2; SEQ ID NO 2; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG36882 standard; protein; 416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                                                                                                                                                                                                                                                                                                     (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                       (KAGA-)
                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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 Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                       KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTAFFLEA 114
                                                                      416
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                                                                                                        ability.
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100.0%; Prr
17.1%; Score 7; DB '100.0%; Pred. No. 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8; Pred. No.
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                                    DB 7;
                   49;
                                    Length 416;
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                                                                                                                                                           for
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<u>.</u>

Indels

<u>.</u>

Gaps

0

Query Match Best Local Matches

Similarity

17.1%; ilarity 100.0%; Conservative (

Score 7; DB 4;; Pred. No. 49; 0; Mismatches

DB 49; 4;

Length 417; Indels

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Gaps

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Sequence

417 AA;

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RESULT 14
AAB92908
ID AAB92
XX Humai
XX 11-
PP 28-
PR 29-
PR 27-
PR 11-
PR 02-
PR 
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                                                                                        cc length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the
cc complementary strand of a polynucleotide which comprises one of the 5602

cc oligonucleotide sequences defined in the specification, where the
cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination
cc of an oligonucleotide comprising a sequence complementary to the
cc complementary strand of a polynucleotide which comprises a 5'-end
cc sequence and an oligonucleotide comprising a sequence complementary to a
cc polynucleotide which comprises a 3'-end sequence, where the
cc oligonucleotide which comprises a 3'-end sequence, where the
cc oligonucleotide comprises at least 15 nucleotides and the combination of
cc the 5'-end sequence/3'-end sequence is selected from those defined in the
cc specification. The primers sets can be used in antisense therapy and in
cc gene therapy. The primers are useful for synthesising polynucleotides,
cc detection and/or diagnosis of the abnormality of the proteins encoded by
cthe full-length cDNAs. The primers are also useful for the
cc detection and/or diagnosis of the abnormality of the proteins encoded by
cthe full-length cDNAs. The primers allow obtaining of the full-length
cc DNAs easily without any specialised methods. AAB03166 to AAB13632 and
cc AAB13633 to AAB13642 represent human cDNA sequences; AAB92446 to AAB3893
cc crigonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-199;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
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, Sugiyama T, Wakamatsu
                                                                   invention
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2000JP-00183767.
2000JP-00241899.
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A, Nagai K,
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C, Otsuki
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AAY49137
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                                                                                                                                                         AAY49137-Y49152 are amino acid sequences that are fragments of choline CCC binding proteins (CBP). The fragments of the protein are the alpha helix CC forming parts of the CBPs from Streptococcus pneumoniae. The polypeptides cCC do not contain the actual choline binding fragment. The polypeptides and the invention, which relates to polypeptide truncates of a pneumococcal curface binding protein containing the highly conserved immunogenic alpha helical portion and no choline binding portion. The polypeptides are used as immunogens in a bacterial vaccine. The vaccine can be used for preventing (immunising) or treating invasive bacterial (especially correventing (immunising) or treating invasive bacterial (caused by pneumococcal) infections, especially obtits media (caused by CAntibodies raised against the polypeptide are useful for detection.

CC prevention (passive immunity) and treatment of S. pneumoniae infections. The vaccine are especially useful in immunocompromised patients, those with an immature immune system, or patients with an on going pneumococcal infection. The vaccine avoids unnecessary expense and provides broad content of supressive and trange of pneumococcal serotypes and it produces an improved and enhanced effect in preventing bacterial infections
                                                                                Query Match
Best Local S
                                                                 Matches
                                                                                                                                 Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 64-65; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pneumococcal proteins useful as vaccines and for diagnosis of pneumococcal infections.
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15-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truncated surface binding protein; alpha helix; choline binding protein; vaccine; invasive bacterial infection; otitis media; sepsis; meningitis; lobar pneumonia infection; antibody; immature immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of choline-binding protein fragment #1.
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                                                               Local Similarity 100 nes 7; Conservative
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                              23 KKEELTS 29
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 KKEELTS 80
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98US-0085743P.
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                                     17.1%; 5---
100.0%; Pred. No. --
1ve 0; Mismatches
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                                                                                DB 2; Length 431; 50;
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Search completed: February 1, 2005, 15:20:12 Job time: 71.7778 secs

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Result
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  222118
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Peq
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length: 2000000000
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1 LKGLFTLFAGHLVKPFADTL.....QVNISKTDEAFFDSENDPEK 41
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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          AAR58611
ADM98779
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ADM98889
AAM14903
AAB3337
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AAM67043
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                  Abb55123 Lactococc
Abb6733 Pseudomon
Abp60399 Yeast HMG
Aar58611 Yeast HMG
Aar58611 Yeast HMG
Aar58611 Yeast HMG-COA r
Adm98798 HMG-COA r
Adm98814 HMG-COA r
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Adm14903 Peptide #
Abb33872 Peptide #
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Abb28688 Peptide #
Abb19311 Protein #
Abb19311 Protein #
Aam67043 Human bra
Aam67043 Human bra
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Abg48708 Human liv
Aam602628 Peptide #
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Aay23793
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Novel pro
Protein e
Human pep
Peptide #
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RESULT 1 AAW54099 ID AAW54099 XX X AC AAW54099 XX DT 28-SEP-1 XX DE Homo sap XX KW BARD1; r XX XX		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	
T 1 099 AAW54099 sta: AAW54099; 28-SEP-1998 Homo sapiens		σ	6	თ	6	σ.	ġ	6	σ	თ	σ	0	σ	σ	6	თ	6	0	6	6	9	
T 1 099 099 AAW34099 standard; protein; 515 AA AAW54099; 28-SEP-1998 (first entry) Homo sapiens BAP28 sequence. BARD1; ring protein; BRCA1; breast						٠			14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6		14.6	
protein; it entry) sequence		144	133	133	133	129	129	121	120	120	118	116	115	115	112	112	85	74	71	65	51	
in;	•	4.	4.	4	4	4	w	ഗ	σ	4	4	ហ	Ф	æ	ហ	w	4.	u	v	7	4	
515 AA.	ALIGNMENTS	AAU17843	ABG22899	AAG80853	AAG83294	AAG80916	AAY52997	ABP38311	ABM71043	AAG81563	AAM51702	ADK36123	ADM98931	ADM98791	ABP00012	AAB41436	ABG02711	ABP02661	ABP03187	ADF07598	ABB44072	
riek;																						
cancer; risk; diagnosis.															Abp00012 Hum	Aab41436 Human	Abg02711 Novel	Abp02661 Human	7		Abb44072 Pep	
			el hum	id bio	P patens	Mitochond	Neisseria	Staphyloc	Staphyloc	S. epider	Human tub	el hum	HMG-CoA r	HMG-CoA r	Human ORF	an ORF	el hum	an ORF	Human ORF	terial	Peptide #	

### 20-SEP-1996; 03-APR-1997; 04-APR-1997; WPI; 1998-230317/20. Bowcock AM, W09812327-A2. Homo sapiens. 19-SEP-1997; 26-MAR-1998. (TEXA ) UNIV AAV24135. Baer R; TEXAS SYSTEM. 96US-0025296P. 97US-0042611P. 97US-0042985P. 97WO-US016842

Disclosure; Page 287-288; 348pp; English.

DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.

The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a BARD1, B123, BE2, BB14, BB31 or BE445 mucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BRCA1, useful to identify a patient having, or at risk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of a BRD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the biological activity of the BRCA1-BARD1,

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(2) (a) an oligo-off primer and an oligonucleotide complementary to the Complementary strand of a polynucleotide which comprises one of the 5602 mucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 mucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end combination CC sequence and an oligonucleotide comprising a sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 1'-end sequence, where the CC oligonucleotide comprises at least 15 mucleotides and the combination of CC oligonucleotide which comprises at least 15 mucleotides and the combination of CC oligonucleotide comprises at least 15 mucleotides and the combination of CC gene therapy. The primer sets can be used in antisense therapy and in the CC gene therapy. The primer sets can be used in antisense therapy and in the CC gene therapy full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length
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AAB92729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T, I
                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-
length CDNAs defined in the specification. Where a primer set comprises
                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used detect BARD1, B123, BE2, BE14, BE31 or BE445, a specific anti-BARD1 antibody can be used to identify a patient having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB92729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HELI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB92729 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELIX RES INST.
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                                                                                                                                                                                                                                                                                                              SEQ
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nilarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                       NO 11159; 2537pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K,
1 A, Nagai K
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RESULT 3
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មិន្ត្រា
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                  The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ghosh
Ma Y,
                                                                                                                                                                                                                                                                                                             New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for ti in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                             Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-569235/53.
N-PSDB; ADE07101.
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
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12-APR-2002; 2002US-0372381P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel gene; novel protein; tissue marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YT, Asundi V, Goodrich
h M, Xue AJ, Wehrman T,
, Wang D, Chen R, Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LKGLFTLFAGHLVKPFADTL 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 1149
                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e AJ,
Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002US-0372615P.
2002US-00128558.
2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                     ID NO 1078; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodrich RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weng G, Z
Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, Zhou F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
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2.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang
10u P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J, Zhao QA,
Drmanac RT,
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Sequence 1149 AA

invention.

DB 7; Length 1149;

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Query Match
Best Local Similarity
Matches 20; Conserv
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Best Local
                                                                                                                                                     The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polynucleotides can be expressed by standard recombinant methodology. BAP28 polynucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first CDNA sequence of the BAP28 gene consisting of the exons 1 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization oppolymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barry C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB85029 standard; protein; 2144 AA
                                                                                                        Sequence 2144 AA;
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18-JAN-2000; 2000US-0176880P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAP28; prostate; tumour; cancer; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by BAP28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 297-304; 349pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF83909,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKGLFTLFAGHLVKPFADTL 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bougueleret L,
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%; Score 20; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Ala or Val
1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Gly or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Asp or Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Ser or Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF83910.
48.8%; Score 20; DB
100.0%; Pred. No. 1.:
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consisting of exons 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen-Akenine
DB 4; Le
1.3e-12;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.7e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                               Length 2144;
  Indels
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Gaps
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RRESULT 5
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ID AAY23793
ID AAY23793
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ID AAY2
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DT 27-A
DT 14-S
XX Iden
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XX JP11
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PR 12-I
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a method for the identification or detection of a microbe, using the gyrase gene as the index. The method involves the use of PCR primers to amplify DNA from the microbe, which is then identified or detected depending on its base sequence. The method can be used to classify and identify an unidentified microbe strain rapidly and with high precision. The present sequence represents a gyrase protein. (Updated on 27-AUG-2003 to correct OS field.)
                   Lactococcus lactis; IL1403
                                                                                                                                                                                 29-AUG-2003
16-MAY-2002
                                                                                                                                                                                                                                                                                                           ABB55123 standard; protein; 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 220 AA;
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14-SEP-1999
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                                                                        Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                               ABB55123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 14-15; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification; detection; microbe; gyrase gene; gyrase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A gyrase protein of Chitinophaga pinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification and detection of a microbe -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 SENDPEK 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKGLFTLFAGHLVKPFADTL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SENDPEK 41
                                                                                                                          lactis protein ysdA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                              (revised)
(first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97JP-00343316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 2; Pred. No. 24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 220;
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RESULT 7
ABO82733
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AC ABO8
XX Pseu
XX Bact
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XX Bact
XX Pseu
XX P
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Best Local
                        N-PSDB; ABD16304.
                                                 WPI; 2003-615309/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and theses. Note: The sequence data for this patent is based on equivalent patent W0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                  Rubenfield MJ,
                                                                                                                                                         (GENO-) GENOME
                                                                                                                                                                                                       18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                   18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                       22-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polypeptide #14908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB082733;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-043418/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000FR-00004630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVNISKT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1825; 2504pp; French.
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                                                                                                                                                   THERAPEUTICS CORP.
                                                                                                                                                                                                                                98US-0074788P
                                                                                                                                                                                                          98US-0094190P
                                                                                                                                                                                                                                                                                   9908-00252991
                                                                                               Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.1%;
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                                                                                            Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                               Bush
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RESULT 8
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Best Local
                                                                                     Increasing squalene and specific sterol accumulation in yeasts - by transforming mutant yeasts to increase 3-hydroxy-3-methyl:glutaryl reductase activity in the yeasts.
                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                    WPI; 1992-168867/21.
N-PSDB; ABZ26037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast; HMG-CoA reductase; squalene; zymosterol; cholesta-7,24-dienol; cholesta-5, 7, 24-trienol; zymosterol-24-methyl transferase; ergosta-5, 7, 24 (28)-trienol-22-dehydrogenase; ergosta; dienol; episterol-5-dehydrogenase; linker region; catalytic domain; membrane binding region; HMG2; enzyme.
                                                                                                                                                                                                                                                                                                             Mukharji I,
                                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5460949-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast HMG2 SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP60399;
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                                                                                                                                                                                                                                                                                                                                                                           (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP60399 standard; protein; 1045 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                                         Saunders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00783861.
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                                                                                                                                                                                                                                                                                                         Wolf FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 7; Pred. No. 56; 0; Mismatches
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Disclosure; Col 63-68; 60pp; English

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RRESULT 9
AAR5861
ID AAR58
XX AAR58
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DT 25-N
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XX Yeas
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XX HMG-
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CC accumulation in yeast comprising increasing the expression level of a
CC structural gene encoding a polypeptide having HMG-CoA reductase activity
CC in a mutant yeast having defects in the expression of zymosterol-24-
CC (B) a method of increasing squalene, ergosta-8, 22-dienol, ergosta-8-enol and ergosta-7-enol accumulation in S. cerevisiae
CC comprising transforming a mutant S.cerevisiae having a defect in the
CC expression of episterol-5-dehydrogenase with a recombinant DNA molecule
CC comprising a vector operatively linked to an exogenous DNA segment that
CC enzyme and a promoter suitable for driving the expression of the
CC enzyme and a promoter suitable for driving the expression of the
CC zymosterol-24-methyl transferase and episterol-5-dehydrogenase with a
CC cerevisiae comprising
CC risholesta-7, 24-dienol accumulation in S. cerevisiae comprising
CC raductase in the yeast, (C) a method of increasing squalene, Zymosterol
CC zymosterol. 4-methyl transferase and episterol-5-dehydrogenase with a
CC cerevisiae having a defect in the expression of
CC cumulation in S. cerevisiae comprising transforming a mutant S.
Ccerevisiae having a defect in the expression of
CC mutant S. cerevisiae comprising transforming a mutant S.
Ccerevisiae having defects in the expression of zymosterol-24-
methyl transferase and ergosta-5, 7, 24(28)-trienol-32-dehydrogenase
CC enzymes, which mutant is designated ATCO402mm; (F) a mutant of S.
CC cerevisiae having single or double defects in the expression of enzymes
CC enzymes the conversion of squalene to expression of the
CC carevisiae having single or double defects in the expression of enzymes
CC enzymes the conversion of squalene to expression of the
CC carevisiae having single or double defects in the expression of enzymes
CC enzymes the conversion of squalene to expression of that of the
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CC conversion of squalene to expression of that of the

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Best Local
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28-APR-1995
WPI; 1994-302280/37
N-PSDB; AAQ70611.
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                                                                                                                               Wolf FR,
                                                                                                                                                                                                                                                                                                           12-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
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                                                                                                                               Saunders CA,
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(first entry)
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100.0%; Pred. No. 94;
tive 0; Mismatches
                                                                                                                               Chappell
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RESULT 10
ADM98779
ID ADM98
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                                                                                                                                                                                                                                                                                                  AAQ70611 codes for a yeast HMG-CoA reductase 2, AAR58611. Using the A. tumefaciens vector pXYLX71, AAQ70611 was used to produce transgenic plants with increased HMG-CoA reductase activity. Plants with increased HMG-CoA reductase activity were found to have greater squalene and sterol accumulation, and therefore increased insect resistance. (Updated on 25-MAR-2003 to correct PF field.)
                                ADM98779
                                                                                                                                                                                                                                                                      Sequence 1045 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plants with increased insect resistance - by transformation with DNA encoding HMG-CoA activity to increase squalene and sterol
 01-JUL-2004
                                                            ADM98779 standard; protein; 1045 AA.
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(first entry)
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Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-COA reductase; enzyme. US2004072323-A1 05-JAN-2001; 2001US-0259880P 07-JAN-2002; 2002US-00041018 Saccharomyces cerevisiae. HMG-CoA reductase polypeptide #32. (MATS/) MATSUDA S P T. (HART/) HART E A. 15-APR-2004.

The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a diterpene or diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic the cells. New unicellular organisms comprising exogenous nucleic acids encoding a geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors. Disclosure; SEQ ID NO 199; 38pp; English

cells further comprises at least one isolated and d sequence of a yeast expression library, and the e

WPI; 2004-373921/35. Matsuda SPT, Hart EA;

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RESULT 11
ADM98798
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                                                                                                                  The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence is regulated by an inducible promoter under conditions where the expression is induced, filtering the cell/resin mixture, extracting the cell/resin mixture with alcohol to produce an organic eluent and analysing the organic eluent by a screening method including chromatography and/or spectroscopy, to identify the nucleic acid sequence encoding the diterpene synthase. The unicellular microorganism is useful as a diterpene or diterpene precursor producing system. Diterpenes, in plants, serve as defence toxins, volatile defensive signals, pollinator attractants and photoprotectants. This sequence represents an HMG-COA reductanse polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from
the organism. The invention also relates to methods of producing a diterpene or diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of the cells further comprises at least one isolated and purified mucleic acid sequence of a yeast expression library, and the expression of the
                                                                                                                                                                                                                                                                               geranylgeranyl pyrophosphate and a producing diterpenes and diterpene
                                                                                                                                                                                                                                                                                                  New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for
                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 218; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Matsuda
                                                                                                                                                                                                                                                                                                                                                                                                                                              (MATS/) MATSUDA S P T. (HART/) HART E A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMG-CoA reductase polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attractant; photoprotectant;
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larity 100.0%; Pred. No. 94
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Hart EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrophosphate synthase; diterpene; diterpene precursor;
hase; defence toxin; volatile defensive signal;
ractant; photoprotectant; HMG-CoA reductase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                 precursors
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                                                                          conditions where the expression is induced, filtering the cell/resin mixture, extracting the cell/resin mixture with alcohol to produce an organic eluent and analysing the organic eluent by a screening method including chromatography and/or spectroscopy, to identify the nucleic acid sequence encoding the diterpene synthase: The unicellular microorganism is useful as a diterpene or diterpene producing system. Diterpenes, in plants, serve as defence toxins, volatile defensive signals, pollinator attractants and photoprotectants. This sequence represents an HMG-COA reductants and photoprotectants the sequence represents an HMG-COA reductants and photoprotectants from the invention. Note: The sequence data for this patent did not form part of the printed specification but was betained in electronic format from
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                         Similarity 7; Conserv
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HLVKPFA
                          Conservative
                                17.1%;
                         Score 7; DB 8; Pred. No. 94; 0; Mismatches
                             DB 94;
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                          <u>.</u>
                                      Length 1045;
                          Indels
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RESULT 12

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ADM98844
                                                                                            ADM98844;
                                                                                   HMG-CoA reductase polypeptide
                                                                                        01-JUL-2004
                                                                                                ADM98844 standard; protein; 1045
                                                                                       (first entry)
                                                                                   #97.
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Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-COA reductase; enzyme.

Saccharomyces cerevisiae.

US2004072323-A1

15-APR-2004

07-JAN-2002; 2002US-00041018.

05-JAN-2001; 2001US-0259880P

(MATS/) MATSUDA S P (HART/) HART E A.

SPT,

WPI; 2004-373921/35.

New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors

Disclosure; SEQ ID NO 264; 38pp; English

The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic a yeast expression library,

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RESULT 13
ADM98916
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The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a diterpene precursor and a method of isolating a diterpene synthase compristing growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of the cells further comprises at least one isolated and purified nucleic
                                                                                                                                                                                                                                                                                                                                                                                                              New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-373921/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsuda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004
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HART E A.
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                                                                                                                                                                                                                                                                                                                                                                                   diterpenes and diterpene precursors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anyl pyrophosphate synthase; diterpene; diterpene precursor;
synthase; defence toxin; volatile defensive signal;
attractant; photoprotectant; HMG-CoA reductase; enzyme.
                                                                                                                                                                                                                                                                                                                                  SEQ ID
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RESULT 14
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         The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a diterpene or diterpene precursor and a method of islating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of the cells further comprises at least one isolated and purified nucleic the cells further comprises at least one isolated and purified nucleic
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                                                                                                                                                                                                                                               New unicellular organisms comprising exogenous nucleic acids encoding a geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
                                                                                                                                                                                                                                                                                                                                                                Matsuda SPT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.
                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-2001; 2001US-0259880P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMG-CoA reductase polypeptide #142
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(HART/) HART E A.
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7; Conserv
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100.0%;
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RESULT 15
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Best Local S
Matches 7
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          The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                   Penn
                                                                                                                                                 Claim 27;
                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                    WPI; 2001-488901/53
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer.
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                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                 SEQ ID NO 19729; 487pp; English.
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; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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larity 100.0%; Pred. No. 94
Conservative 0; Mismatches
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Note:

The sequence data for this patent did not

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SSSS
Sequence 45 AA;
                                      part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Query Match Best Local Similarity Watches 6; Conservi á 18 DTLDQV Conservative 23 14.6%; Score 6; DB 4; Pred. No. 70; 0; Mismatches 0 DB 70; 4. <u>.</u>. Length 45 Indels 0 Gaps

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Search completed: February 1, 2005, 15:20:16. Job time: 72.7778 secs

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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

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      GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
                                              US-09-270-767-33214
US-09-270-767-48431
US-09-513-999C-5558
US-09-513-99C-6450
US-09-513-99C-64616
US-09-540-236-3312
US-09-248-796A-2528
US-09-270-767-35660
US-09-270-767-36390
US-09-270-767-38390
US-09-270-767-38390
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US-08-446-908-2
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US-08-231-205A-2
US-08-871-161-2
US-08-486-908-2
US-08-248-796A-19869
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US-09-248-796A-18839
                   US-09-248-796A-14685
US-08-685-992-10
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Sequence 33214, A
Sequence 48431, A
Sequence 5558, Ap
Sequence 4172, Ap
Sequence 4616, Ap
Sequence 25228, A
Sequence 33660, A
Sequence 33607, A
Sequence 53607, A
Sequence 53607, A
Sequence 53607, A
Sequence 2195, A
Sequence 27, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 23, Appli
Sequence 260, Appli
Sequence 19639, A
Sequence 16711, A
Sequence 1685, A
Sequence 16839, A
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
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17 VPVLNTA 23

Query Match Best Local S: Matches 7	RESULT 2 US-09-270-767-48431 ; Sequence 48431, Appli: patent No. 67034701 ; GENERAL INFORMATION: ; APPLICANT: Homburger ; TITLE OF INVENTION: ; FILE REFERENCE: File ; CURRENT APPLICATION IN CURRENT FILING DATE: ; NUMBER OF SEQ ID NOS ; SOFTMARE: Patentin V. ; SEQ ID NO 48431 ; LENGTH: 160 ; TYPE: PRT ; ORGANISM: Drosophil US-09-270-767-48431	Query Match Beet Local Si Matches 7; Qy 17 V Db 52 V	RESULT 1 US-09-270-767-3321 Sequence 33214, Patent No. 67034 GENERAL INFORMAT APPLICANT: Homb ITILE OF INVENT: FILE REFERENCE: CURRENT APPLICA CURRENT APPLICA CURRENT FILING NUMBER OF SEQ I SOFTWARE: Paten SEQ ID NO 33214 LENGTH: 160 TYPE: PRT ORGANISM: Dros US-09-270-767-3321		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
similarity 1 Similarity 1 7; Conservati	767-48431 0. 6703491 INFORMATION: INT: Homburger et al. INT: HOMBURGER et al. PINURN'ION: Nucleic FERENCE: File Refere APPLICATION NUMBER: FILING DATE: 199-0 OF SEQ ID NOS: 62517 E: Patentin Ver. 2.0 0. 48431 16.0 1767-48431	milarity Conservat PVLNTA 23 	Appli 91 100: 100: 100: 100: File TION DATE: D NOS tin V		144.66 329 144.66 329 144.66 330 344.66 334.33 37 37 37 37 37
17.1%; 100.0%; ive	cet al. Nucleic acids Reference: 7 NUMBER: US/09 1999-03-17 1999-03-17 2012 Numer: 2.0	17.1%; 100.0%; ive	ccation US/092 et al. Nucleic acids Reference: 7: NUMBER: US/09, 1999-03-17 162517 /er. 2.0		444344444444444444444444444444444444444
Score 7; DB 4; Pred. No. 8.3; 0; Mismatches	US/09270767  acids and proteins nce: 7326-094  US/09/270,767 3-17	Score 7; DB 4; Pred. No. 8.3; 0; Mismatches	US/09270767  acids and proteins nce: 7326-094 US/09/270,767	ALIGNMENTS	US-09-540-236-3779 US-09-134-000C-5845 US-09-489-039A-8203 US-09-134-001C-3551 US-09-149-476-483 US-09-149-476-483 US-09-149-796A-16383 US-08-454-196-17 US-08-454-196-17 US-09-248-796A-16176 US-09-291-046-17 US-09-291-046-17 US-09-248-796A-16176 US-08-683-262B-64 US-09-361-707-64 US-09-3150-133-5 US-09-150-141-5
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US-09-513-999C-5558

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US-09-621-976-6450
; Sequence 6450, Application US/09621976
; Patent No. 6639063
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; LENGTH: 61
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4172
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/107,433
PRIOR APPLICATION NUMBER: US 60/107
PRIOR APPLICATION NUMBER: US 60/107
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; ORGANISM: Homo sapiens
US-09-513-999C-5558
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Best Local (
                                                                                                                                                                                      Matches
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5558
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4172, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.6%; Score 6; 18est Local Similarity 100.0%; Pred. No. Matches 6; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR RILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PATHOO-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
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les 6; Conservative
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                                                                                                               LLCKNF 16
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6783961
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; LOCATION: 22
; OTHER INFORMATION: Xaa=Cys or
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; ORGANISM: Homo sapiens
US-09-621-976-6450
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6783961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: SIGNAL
LOCATION: -48..-1
OTHER INFORMATION: 6
OTHER INFORMATION: 6
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Best Local Similarity
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SEQ ID NO 6450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                 NAME/KEY: UNSURE
                                                                                                                                               LOCATION: 21
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 19335
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                                                                                                                                                                                                                        NAME/KEY: UNSURE LOCATION: 8
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 87
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              Conservative
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       14.6%; Score 6; DB 4
100.0%; Pred. No. 55
tive 0; Mismatches
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US-09-540-236-3312
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US-09-248-796A-25228
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US-09-248-796A-25228
Sequence 35660, Application US/09270767
Patent NO. 6703491
GEMERAL INFORMATION:
GEMERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GATY L. BYETON et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/19/248,796A
CURRENT FILING DATE: 1999-02-12
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SEQ ID NO 3312
LENGTH: 98
TYPE: PRT
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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25228
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Best Local
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Patent No. 667391
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Best Local Similarity
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TYPE: PRT
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100.0%; Pr
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Query Match
Best Local Similarity
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US-09-270-767-50877; Sequence 50877; A
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                                                                         ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-38390
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US-09-270-767-38390
; Sequence 38390, Application US/09270767
; Patent No. 6703491
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38390
LENGTH: 127
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 50877
LENGTH: 99
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35660
LENGTH: 99
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GENERAL INFORMATION:
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OTHER INFORMATION: Xaa means any amino acid
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RESULT 13
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US-09-270-767-53607
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US-09-248-796A-22195
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22195
LENGTH: 135
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE OF ENVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE OF ANDRER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 53607

LENGTH: 127

TYPE: PRT
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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TITLE OF INVENTION: ADOPTIVE IMMUNOTHERAPY WITH INTERLEUKIN-7
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-09-710-279-1214
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Search completed: February
Job time : 17.5556 secs
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US-09-710-279-1214
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CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1214
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Patent No. 6703492
GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
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TYPE: PRT
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Maximum DB seg length: 2000000000
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(without alignments)
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gn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US09NEW_PUB.pep:*
gn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US10EW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

## SUMMARIES

11210987654221	Result No.
41 77 77 77 77 77	Score
100.0 177.1 177.1 177.1 177.1 177.1 177.1 177.1 144.6	Query Match Length DB
1149 1045 1045 1045 1045 1045 1045 1045 1045	ength I
115 115 115 115 115 115 115 115 115	E
US-10-128-558-167 US-09-823-829-6 US-09-823-829-6 US-09-823-823-6 US-10-041-018-19 US-10-041-018-264 US-10-041-018-36 US-10-041-018-36 US-10-041-018-36 US-10-041-018-39 US-10-041-018-39 US-10-041-018-39 US-10-041-018-39	ID
Sequence 167, App Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1836, Ap Sequence 199, App Sequence 214, App Sequence 201, App Sequence 309, App Sequence 307, App Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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3-86	-10-788-792-	-10-425-114-	-10-767-701-4419	-10-424-599-	-10-739-930-	US-10-154-251-40	-10-056-884-	-10-425-115-200	-10-425-114-433	-10-424-599-14835	-425-115-	-10-424-599-1	-10-425-115-34227	-10-425-115-	-10-739-956-	0-767-701-	-10-437-963-	-10-424-599-17736	-10-041-018-3	-10-041-018-	-10-425-115-	-10-424-599-24415	-10-424-599-1573	US-10-767-701-46828	US-10-424-599-182753	-10-424-599-26994	5-115-25058	US-10-425-115-237591	0-424-599-14318	34	0-424-599-2845
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
S	65,	67793, A	4196,	249118,	υį		6, Appli	2	43393, A	148350,	351501,	174950,	342272,	194350,	10, Appl	56103, A	114015,	177366,	, Ap	211, App	340045,	244159,	157320,	828	275	269946,	950	237591,	4318	3471	84582,

### ALIGNMENTS

RESULT 1
US-10-128-558-167
; Sequence 167, App
; Publication No. PRIOR APPLICATION NUMBER: US 60/339,453
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 99/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22 GENERAL INFORMATION: FILE REFERENCE: 812A
CURRENT APPLICATION NUMBER: US/10/128,558
CURRENT FILING DATE: 2002-04-22 APPLICANT: Drmanac, Radoje T TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides APPLICANT: Tang, Y. Tom APPLICANT: Wang, Zhiwei APPLICANT: Weng, Gezhi PRIOR PRIOR PRIOR APPLICATION NUMBER: US 09/560,875
FILING DATE: 2000-04-27
APPLICATION NUMBER: PCT/US01/03800
FILING DATE: 2001-02-05 APPLICATION NUMBER: PCT/US01/02623 FILING DATE: 2001-01-25 APPLICATION NUMBER: US 09/496,914 APPLICATION NUMBER: US 09/515,126 FILING DATE: 2000-02-28 FILING DATE: 2000-02-03 APPLICATION NUMBER: US 09/491,404 FILING DATE: 2000-01-25 Boyle, Bryan J Application US/10128558 US20040219521A1 Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 412

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US-10-128-558-167
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Kasai, Hiroaki
APPLICANT: Hamada, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS
TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR
FILE REFERENCE: 12817-004001
CURRENT APPLICATION NUMBER: US/09/823,829
CURRENT FILING DATE: 2001-03-30
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Sequence 193489, Application US/10437963
Publication No. US20040123343A1
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SEQ ID NO 167
LENGTH: 1149
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-10-437-963-193489
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                                                                                                                                            APPLICANT: Yamamoto, Satoshi
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Kasai, Hiroaki
APPLICANT: Hamada, Tohru
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
RUNNERN OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(182)
OTHER INFORMATION: unsure at all Xaa locations
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FEATURE:
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Sequence 1836, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US/0/360,039
PRIOR FILING DATE: 2002-02-21
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: JP 9:
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin version 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SUZUKI, MAKOTO
APPLICANT: Hamoda, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING G)
IITLE OF INVENTION: GENE AS AN INDICATOR
FILE REFERENCE: 12817-004001
CURRENT APPLICATION NUMBER: US/09/823,823
CURRENT FILING DATE: 2001-03-30
PRIOR FILING DATE: 1998-12-10
PRIOR PILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 80
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APPLICANT: Kasai, Hiroaki
APPLICANT: Nakamura, Shoko
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TYPE: PRT
Chitinophaga pinensis
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100.0%; Pred. No. 39
tive 0; Mismatches
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NUMBER OF SEQ SEQ ID NO 1836

IJ

NOS: 47374

ENGTH:

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                                    Query Match
Best Local Similarity
"hes 7; Conserv?
                                                                                                                  LENGTH: 1045
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-041-018-218
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Publication No. US20040072323A1

GENERAL INFORMATION:
APPLICANT: Mateuda, Selichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                      Sequence 218, Application No. US200 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 199
LENGTH: 1045
                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 218
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                                                                                                                                                                                                               APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: PO2080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
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11 HLVKPFA 17
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                                                  17.1%; Score 7; DB
100.0%; Pred. No. 1.
:ive 0; Mismatches
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RESULT 10
US-10-041-018-336
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               Sequence 336, Application US/10041018
Publication No. US20040072323A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 309, Application US/10041018
Publication No. US20040072323A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
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APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
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Publication No. US20040072323A1
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Best Local
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Matches 7; Conserv
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TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547

CURRENT APPLICATION NUMBER: US/10/041,018

CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: US 60/259880

PRIOR APPLICATION NUMBER: US 60/259880

PRIOR APPLICATION NUMBER: US 60/259880

PRIOR PILING DATE: 2001-01-05

PRIOR PILING DATE: 2001-01-05

PRIOR PILING DATE: 2001-01-05
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SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
CURRENT APPLICATION NUMBER: US/10/041,018
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1045
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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o. 1.6e+02;
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TOPOLOGY: UNKNOWN

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-879-957-79
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US-09-879-957-79
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Best Local Similarity
                   Query Match
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PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
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TYPE: PRT
                                                                                                                                                                                    TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 79: SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
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Local Similarity 100.0%; Pred. No.
hes 7; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-JUN-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Pennie
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HOFFMAN, NO. US20020034755A1h
KAY, Brian K.
FOWLKES, Dana M.
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STATE: New York
                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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14.6%; Score 6; DB 9;
100.0%; Pred. No. 91;
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o. 1.6e+02;
                      Length 41;
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US-09-864-761-47882

Sequence 47882, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

RESULT 13

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Matches
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Publication No. US20040157216A1
GENERAL INFORMATION:
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                                                                                                  Query Match
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                                                                                    Local
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/807,856
FILING DATE: 23-Mar-2004
CLASSFECATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                      MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SPARKS, Andrew B.
29
                       36 ENDPEK 41
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                                                                Similarity 6; Conserv
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ENDPEK 34
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                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
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                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                          ENGTH: 41 amino acids
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                                                                  Conservative
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                                                                                  14.6%;
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                                                                  ; Score 6; DB 1
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0; Mismatches
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                                                                                    DB 16;
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                                                                                                  Length 41;
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avid R. David K.

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US-10-424-599-284582

Sequence 284582, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7

OTHER INFORMATION: EST HUMAN HIT: AU132001.1, EVALUE 7.00e-23

OTHER INFORMATION: SWISSPROT HIT: P04035, EVALUE 6.00e-24

US-09-864-761-47882
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SEQ ID NO 47882
LENGTH: 51
TYPE: PRT
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Best Local (
APPLICANT: La Rosa Thomas J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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IITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
IITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
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Search completed: February Job time: 59.7778 secs

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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 53471
LENGTH: 69
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
FEATURE:
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US-10-767-701-53471
; Sequence 53471, Application US/10767701
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_99002C.1.pep
US-10-424-599-284582
                                                                                                                              ; OTHER INFORMATION: Clone ID: 13392228.pep US-10-767-701-53471
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 284582
SEQ ID NO 284582
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ALIGNMENTS	A64790	D85555	A90705	F83097	B47080	T35202	G83293	AG2653	C97435	D98060	G95193	G91265	D86106	AD1022	H65220	B40656	
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#### hypothetical protein CC0498 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004 C;Accession: A87311 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.: B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolond, n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Status: preliminary A;Status: preliminary 밁 8 A;Cross-references: UNIPROT:Q9AAU6; GB:AE005673; NID:g13421677; PIDN:AAK22485.1; GSPDB:GI C;Genetics: A; Gene: A; Molecule type: DNA A; Residues: 1-296 < STO> Matches Query Match Local CC0498 240 LFTLFAG 246 4 LFTLFAG 10 h 17.1%; Score 7; DB Similarity 100.0%; Pred. No. 7; Conservative 0; Mismatches *ا*د Length 296; <u>;</u> Indels 0; Gaps 0;

conserved hypothetical protein VC1339 [imported] - Vibrio cholerae (strain N16961 serogro (;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Ju1-2004
C;Accession: C82213
R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82213

RESULT C82213

A; Molecule type: DNA
A; Residues: 1-400 <HEI>
A; Cross-references: UNIPROT: Q9KSB9; C
A; Experimental source: serogroup O1; C; Genetics:

GB:AE004213; GB:AE003852; NID:g9655819; PIDN:AAF9449; strain N16961; biotype El Tor

A;Gene: VC1339
A;Map position: 1
C;Superfamily: uncharacterized conserved

protein

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hydroxymethylglutaryl-CoA reductase N;Alternate names: protein 19324.2; C;Species: Saccharomyces cerevise C;Date: 28-Feb-1990 #sequence revisi C;Accession: B30239; B24317; $55972
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R;Mierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolorin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
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A; Residues: 1-453 <STO>
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A;Accession: F86846
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                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3C transporter permease protein ysdA [imported] - Lactococcus lactis subsp. ;pecies: Lactococcus lactis subsp. lactis;pate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: DNA
;Residues: 1-422 <STO>
;Cross-references: UNIPROT:Q9A5L8; GB:AE005673; NID:g13423972; PIDN:AAK24400.1;
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;Accession: D87550
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               revision 28-Feb-1990 #text_change 09-Jul-2004
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0; Mismatches
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0; Mismatches
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Pred. No.
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hypothetical protein ECs0765 [imported] - Escherichia coli (strain O157:H7, subs C/Species: Escherichia coli
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: E90724
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Reference number: A99829; MUID:21156231; PMID:11258796
                                                                                                                                                                  A;Cross-references: UNIPROT:Q8X982; GB:BA000007; PIDN:BAB34188.1; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-55 <HAY>
                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                      A; Reference number: A99629; A; Accession: E90724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, March 1995 A; Description: The sequence of S. cerevisiae of A; Reference number: $55966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: SGD:S0004442; MIPS:YLR450w A;Map position: 12R
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Proc. Natl. Acad. Sci. U.S.A. 83, 5563-5567, 1986
A;Title: Saccharomyces cerevisiae contains two functional
A;Reference number: A94112; MUID:86287298; PMID:3526336
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A; Residues: 1-1045 < CBAS>
A; Cross-referes: UNIPROT: P12684;
A; Cross-references: UNIPROT: P12684;
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C; Superfamily: hydroxymethylglutaryl-CoA reductase I
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A; Residues: 772-961 <BAS2>
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A;Title: Structural and functional conservation between A;Reference number: A93105; MUID:89127221; PMID:3065625
A;Accession: B30239
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6; Conser
TLNOVN 24
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100.0%; Pr
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TLNOVN

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C;Accession: F75451

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans lA;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: F75451
               conserved hypothetical protein VCA0152 [imported] - Vibrio cholerae (strain N16961 (;Species: Vibrio cholerae
(;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82494
C;Accession: E82494
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selle
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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A;Experimental source: strain R1
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A; Residues: 1-75 < WHI>
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R;Perna, N.T.; Pluni
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pathogen Vibrio cholerae.
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                                                               Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
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K.; Apodaca,
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C;Genetics:
A;Gene: SA1356
A;Gene: SA1356
C;Superfamily: Bacillus subtilis conserved hypothetical protein
                                                                                                                                                                                                       R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89932
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
E89932
                                                                                                                                                                                                                                                                                                                                          C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89932
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C;Superfamily: Chlorella virus PBCV-1 hypothetical
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A; Residues: 1-107 < HEI>
                                                                                                              A;Cross-references: UNIPROT:Q99TW8; GB:BA000018; PID:g13701324; PIDN:BAB42618.1; GSPDB:GNA;Experimental source: strain N315
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A;Experimental source: specific host Chlorella strain NC64A
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
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                                                                                                                                                     A; Residues: 1-120 < KUR >
                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein SA1356 [imported] -
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A;Residues: 1-108 <GRA>
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R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A; Winters, P.; Mipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phage-related protein homolog yqbL - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69947
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein BH1707 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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A;Experimental source: strain C-125
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A; Residues: 1-131 <STO>
                                                                                                                                                                                                                                                                                                    ;Cross-references: UNIPROT:P45928; GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14548
;Experimental source: strain 168
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                                                            FDSEND 100
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100.0%; Pred. No. 39
ive 0; Mismatches
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A;Title: Multiple outer membrane receptors for uptake of A;Reference number: S59503; MUID:96069713; PMID:7476877 A;Accession: S59507
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                                                                                                             A; Molecule type: DNA
A; Residues: 1-173 < KOS>
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R;Koster, M.; Ovaa, W.; Bitter, W.; Weisbeek,
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                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                         Mol. Gen. Genet.
                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:047204; EMBL:U79222; NID:g2827789; PID:g2827790; PIDN:AAB9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-162 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: ndhF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T17044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description:
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                                        Matches
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Best Local
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   3 GLFTLF 8
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mber: Z17939
                                        Conservative
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Pred. No. 47;
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50;
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                          Database :
                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        Word size :
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                           1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                          SEQ5ALA1854
41
1 EKNWKNHMGPFMSILQEHIG.....MKKEELTSHQSQLTAFFLEA 41
UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result

		*			000000000000000000000000000000000000000	
esult No.	Score	Query	Length	DB		cription
1	41	100.0	349	2	Q96ES5	Q96es5 homo sapien
N	41	00.	897	N	Q8N7L7	717 homo
ω	41	80.	1106	N	Q6P197	7 homo
4	41	00.	1106	N	AAH65205	05 homo
v			958	<b>-</b>	BP28_MACFA	maca
თ		<b>в</b>	2144	_	BP28_HUMAN	
7	19	9	349	N	Q8VCK1	mus r
8	19	٥.	408	N	QBCCT5	Q8cct5 mus musculu
9	8		163	N	Q8BIC5	5 mus
10	8	•	354	N	Q8BIJ2	
1	0	19.5	445	N	Q7N5B2	N
12	8	•	448	N	Q7NRX0	_
13	8	•	453	N	Q98DW1	
14	. 00	19.5	454	N	Q87H28	Q87h28 vibrio para
15	. 00	•	462	N	Q7WBI0	_
16	8	•	462	N	Q7WN02	
17	8		462	N	Q8XQI3	Q8xqi3 ralstonia s
18	8		465	N	086080	
19	8		465	N	Q89NV6	
20	80		465	N	Q8P701	
21	8		467	N	Q8Z912	
22	8		467	N	Q8ZRG3	~
23	8		468	N	Q6N0G9	Q6n0g9 rhodopseudo
24	8	•	468	ผ	Q73H35	ĕ
25	8		468	N	CAE30233	233 rhodopse
26	8	٠	468	N	AAS14431	3
27	00	•	469	N	Q8PG82	Q8pg82 xanthomonas
28	8	•	471	N	Q8P4L6	
29	8	19.5	478	N	Q88E17	
30	8		479	N	Q87WA6	
31	8	19.5	487	N	Q8PIBS	Q8pib5 xanthomonas

32 8 19.5 488 2 O07440 33 8 19.5 488 2 Q7DC90 34 8 19.5 493 2 Q92S67 35 7 17.1 258 2 Q88E22 36 7 17.1 417 2 Q9NVT4 37 7 17.1 460 2 Q7S9N1 38 7 17.1 464 2 Q8NVT5 39 7 17.1 482 2 Q8ZG5 40 7 17.1 525 2 Q8ZG5 41 7 17.1 525 2 Q8ZG5 42 7 17.1 527 1 CYDA AZOVI 42 7 17.1 545 2 Q9RUT4 42 7 17.1 545 2 Q9RUT4 43 7 17.1 545 2 Q9RUT4 44 7 17.1 667 2 Q9RUT4 45 7 17.1 739 .2 Q9RUT4	8 19.5 488 2 0 8 19.5 488 2 0 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
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	2 007440 2 Q7DC90 2 Q92S67 2 Q98E22 2 Q9NVT4 2 Q7Z9N1 2 Q8XQL5 2 Q8XQL5 2 Q8XQL5 2 Q8GZT5 2 Q8GZT6 1 CYDA_AZOVI 2 Q9RVT4 2 Q9RVT4
2 Q07440 2 Q07569 2 Q92667 2 Q98E22 2 Q98WY14 2 Q7Z9N1 2 Q8WKT5 2 Q8XGL5 2 Q8XGL5 2 Q8GZI5 2 Q8GZI5 1 CYDA_AZOVI 1 CYDA_AZOVI 2 Q9KZ28 2 Q9KZT4	IAOZ
007440 Q7DC90 Q92567 Q98E22 Q9NVT4 Q72N1 Q72N1 Q8NKT5 Q8XQL5	IAOZ
	0074490 Q7dc90 Q92867 Q88e22 Q9nvt4 Q7z9n1 Q8xq15 Q8xg15 Q8gzt5 Q8gu5 Q89049 Q6bu55 Q96bu56

# ALIGNMENTS

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EKNWKNHMGPFMSILQEHIGAMKKEELTSHQSQLTAFFLEA	MATCHES 41; CONSERVATIVE 0; MISMATCHES 0; INCELS 0; GAPS 0;	atch 100.0%; Score 41; DB 2; Length 349; cal Similarity 100.0%; Pred. No. 1.9e-36;	SEQUENCE 349 AA; 39921 MW; 3A359597FF7079EB CRC64;	1983.1;	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.		[2] SEQUENCE FROM N.A.	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.":	Marra M.A.;	Schmutz J., Myers R.M., Butterfield	man J.W., Green B.D., Dickson M.C.,	Faney J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		J., Usdin T.B., Toshiyuki S., Carninci P.,	M A	F., Jordan H., Moore T., Max S.I., Wang J., Hsie	K.H., Schaefer C.F., Bhat N	R D. Colling F.S. Wagner I. Shenmen C.M.	MEDLINE=22388257; PubMed=12477932; Strausherg R.L Feingold R.A Grouse L.H Derge J.G		SEQUENCE FROM N.A.	NCBI_TaxID=9606;	alia; Eutheria; Primates; Catarrhini; Hominidae;	Chordata;	Name=FLOIDSDY;	in.	(TrEMBLrel. 25,	2001 (TrEMBLrel. 19, Creat	96ES5;	UYOBSS PRELIMINARY; PRT; 349 AA.	RESULT 1

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RESULT
Q6P197
ID Q6P197
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AC Q6
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DT 05
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DT N5
DT N8
OS HC
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RA Ota T., Suzuki Y., Mishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Anon Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aoteuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami S.,
RA Kawabama S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Kawabama A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima S., Satoh T., Nahizuno T., Morinaga M., Sasaki M.,
RA Mizushima S., Satoh T., Shirati Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Okumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Okimari R., Kawakami T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Okumura K., Yada T., Nahamara Y., Ohara O., Isogai T., Sugano S.,
RA Okumara M., Satoh T., Shirati Y., Takahashi Y., Nakagawa K.,
RA Mishima M., Satoh T., Shirati Y., Takahashi Y., Nakaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                             Q6F197 PRELIM
Q6F197;
Q6F197;
Q5-UUL-2004 (TrEMB
05-UUL-2004 (TrEMB
05-UUL-2004 (TrEMB
FLJ10359 protein (
Name=FLJ10359;
         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 36:40-45(2004).
EMBL; AK098212; BAC05261.1; -.
InterPro; IPR008938; ARM.
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                                                                                                                 (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation updato
ctein (Fragment).
                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                   (Human).
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   Chordata;
Primates;
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Last sequence update)
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                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2;
Pred. No. 4.4e-3
; Mismatches
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                      PRT;
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RESULT 4
AAH62
ID 62-N
DT 02-N
RA NCBI
RA Stag
RA Hoph
RA Diat
RA Stag
RA BOOR
RA RAhg
RA BOOR
RA RAhg
X MEDLINE=22388257; PubMed=12477932;
X MEDLINE=22388257; PubMed=12477932;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X A Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
XA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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XA Altschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
XA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XA Brands S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
XA R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XA RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
XA RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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R Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Toshiyuki S., Casnunci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson K.D., Mullahy S.J.,

RA Rosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richardes S., Woorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;
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02-MAR-2004 (TrEMBLrel. 27, 0
02-MAR-2004 (TrEMBLrel. 27, 1
02-MAR-2004 (TrEMBLrel. 27, 1
FLJ10359 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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Submitted (JAN-2004) to the
EMBL; BC065205; AAH65205.1;
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Proc. Natl. Acad. Sci. U.S.A.
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Primates;
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Last sequence update)
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Pred. No. 5.3
0; Mismatches
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Best Local S
Matches 20
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Best Local Similarity
Matches 41; Conserv
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Q9GM44;
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                         NON TER
                                                                                                                                                                                                                                                                                                                                  libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae;
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16-OCT-2001 (Rel. 40,
01-OCT-2004 (Rel. 45,
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                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=BAP28;
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                                                                                                                                             InterPro; IPR008938; ARM.
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EKNWKNHMGPFMSILQEHIG
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958
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larity 100.0%;
Conservative
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                                                    Score 20;
Pred. No.
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N; 3DBD95C3623CFB31 CRC64;
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Pred. No. 5.3e-36;
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RESOLUTION OF THE RESOLUTION O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HS83; Q9NW23;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
05-JUL-2004 (Rel. 4
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BP28 1
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                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
-!- SIMILARITY: Belongs to the BAP28 family.
-!- SIMILARITY: Contains 1 HEAT repeat.
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Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1534-2144 FROM N.A. Cobley V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   EMBL; AX067150;
EMBL; AL136105;
                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bougueleret L., Chumakov I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein BAP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A novel BAP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         el BAP28 gene and protein.";
number WO0100669, 04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF 1777-2144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OCT-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
      CAC15948.1;
                                  CAC26776.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40, Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND VARIANTS SER-1694; ALA-1854; ASP-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barry C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Irie R.,
, Makita H.,
T., Ishii S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kikkawa E.,
                                                                                                                                                                                                                                                                         a collaboration -
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                                                                                                                                         ch/announce/
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                                                                                                                                                                                                                                                                                                                 A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hong L., Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,

A Hitlanon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.D., Dickson M.C.,

A Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S. J. Marra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8VCK1;
Q8VCK1;
01-MAR-2002
                                                                          Submitted (DE
                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC019693 protein.
Name=BC019693;
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                                                                                                                         STRAIN=mix FVB/N;
TISSUE=Mammary tumor.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932
Strausberg R.L., Feingold E.A., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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REPEAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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     ; BC019693; AAH19693
MGI:2384983; BC0196!
rPro; IPR008938; ARM
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IPR000357; HEAT
                                                                          (DEC-2001) to the
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1694
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                         BC019693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1694
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%;
100.0%;
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                                                                                                                      WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WAP-TGF alpha model. 7 months
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                             EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1853
                                                                                                                                                                                                                              99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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W; D66816EE78D8C9B7
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J.E.,
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                                                                 STRAIN-C57BL/G; TISSUE-Olfactory brain;
STRAIN-C57BL/G; TISSUE-Olfactory brain;
STRAIN-C57BL/G; TISSUE-Olfactory brain;
Shibata K, Itoh M, Aizawa K, Negaoka S, Sasaki N, Carninci P, Shibata K, Itoh M, Aizawa K, Negaoka S, Tashiro H, Itoh M, Sumi N, Ishii Y, Nakamura S, Hazama M, Nishine T, Harada A, Yamamoto R, Matsumoto H, Sakaguchi S, Ikegami T, Kashiwagi K, Fujiwake S, Inoue K, Togawa Y, Izawa M, Ohara E, Watahiki M, Yoneda Y, Ishikawa T, Ozawa K, Tanaka T, Matsuura S, Kawai J, Okazaki Y, Muramatsu M, Inoue Y, Kira A, Hayashizaki Y, "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                           Genome [6]
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last marcation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430400D06 product:hypothetical ARM repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Y., Konno H., Okazaki Y., Muramatsu M., Hayathizaki Y., "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I wanalysis of the mouse transcriptome based on function, 770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae; Murinae; Mue
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Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RR Sambited (JUL-2001) to the EMBL/GenBank/DDBJ databases.

DR MGD; MGI:2384983; BC019693.

NR InterPro; IPR008938; APM

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Q8BIC5;
01-MAR-2003
STRAIN=C57BI/6J;
STRAIN=C57BI/6J;
STRAIN=20499374, PubMed=11042159;
MEDLINE=20499374, PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Carninci P., Shibata Y., Hayatsu N., Hayashizaki Y.;
KOnno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
KOnno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
"Normalization and subtraction of rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
MEDLINE=21085660; PubMed=11217851;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last snortation update)
Mus musculus 86-derived CD11 +ve dendritic cells cDNA, RI
length enriched library, clone:F730048A22 product:weakly
BA393J16.3 (NOVEL KRAB BOX CONTAINING ZINC FINGER GENE).
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STRAIN=C57BL/6J;
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"High-efficiency full-length cDNA cloning.";
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 4
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                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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Rodentia;
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Pred. No.
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5. 2.9e-12;
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                                                                                                   Shibata K.,
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Best Local S
Matches 8
                                                                                                                 Name=BB114266;
Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Q8BIJ2;
01-MAR-2003
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                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:C330026E23 product:weakly similar to BA393J16.3 (NOVEL KRAB BOX
CONTAINING ZINC FINGER GENE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00096; zf-C2H2; \(\overline{5}\).

Prodom; PD000003; Znf C2H2; \(\overline{5}\).

SMART; SM00355; ZnF C2H2; \(\overline{5}\).

PROSITE; PS00028; ZINC FINGER C2H2 1; \(\overline{5}\).

PROSITE; PS50157; ZINC_FINGER_C2H2_2; \(\overline{5}\).

PROSITE; PS50157; ZINC_FINGER_C2H2_2; \(\overline{5}\).
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STRAIN=C57BL/6J;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P15822; 1BBO.

MGD; MGI:2143362; BB114266.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003676; F:nucleic acid binding;

GO; GO:0008270; F:zinc ion binding; IEA.

InterPro; IPR007087; Znf_C2H2.
                                                                                            NCBI_TaxID=10090;
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STRAIN=C57BL/6J;
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                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                     Chordata;
Rodentia;
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0; Mismatches
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                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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MGD; MGD; MGI:2143362; BB114266.

RGO; GO:0005634; C:nucleus; IEA.
RGO; GO:0005676; F:nucleus; IEA.
RGO; GO:0008270; F:zinc ion binding; IEA.
RGO; GO:000827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; MEDLINE=2049374; PubMed=11042159; MEDLINE=2049374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Carninci P., Shibata Y., Muramatsu M., Hayashizaki Y., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs t prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK049344; BAC33696.1; HSSP; P08046; 1F2I.
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                                                                                                                                                                                                                                                                                                                                transcription, DNA-dependent; IEA
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Best Local
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Q7NRXO;
Q7NRXO;
01-MAR-2004 (TrEMBLrel. 26, Cr)
01-MAR-2004 (TrEMBLrel. 26, La)
01-MAR-2004 (TrEMBLrel. 26, La)
Cyanide insensitive terminal co
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MEDLINE=2957627; PubMed=14528314;
Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
Duchaud E., Rusniok C., Frangeul L., Chandler M., Charles J.-F.,
Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Gaudriault S.,
Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7N5B2;
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PhotoList; plu2043; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photorhabdus luminėscens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to quinol oxidase subunit OrderedLocusNames=plu2043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7N5B2
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SEQUENCE FROM N.A.
STRALN=ATCC 12472 / DSM 30191;
MEDLINE=22882880; PubMed=14500782;
Vasconcelos A.T.R., de Almeida D.F., Hu
Antonio R.V., Almeida F.C., de Almeida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 445 AA
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                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                  Chromobacterium violaceum.
                                                                                                                                                                                                                                           Cyanide insensitive terminal oxidase Name=cioA; OrderedLocusNames=CV3658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Biotechnol. 21:1307-1313(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of the entomopathogenic luminescens.";
                                                                                                                                         NCBI_TaxID=536;
                                                                                                                                                                     Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; GO:0006118; P:electron transport; InterPro; IPR002585; Bac_Ubq_Cox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
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8; Conserv
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da L.G.P., de
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       Guimaraes
e Almeida F
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RA Astcolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Creczyneki-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Creczyneki-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Fariss I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Fartapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA Madeira H.M.F., Mendeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Nascimento F.F., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
Silva A.M.C., Stores R.B.A., Souza E.M., Souza K.R.L.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,
Temarkable and exploitable bacterial adaptability.",
Permarkable and exploitable bacterial adaptability.",
Permarkable and exploitable bacterial adaptability.",
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Q98DW1;
01-OCT-2001
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Pfam; PF01654; Bac_Ubq_Cox; 1.

Complete proteome; Oxidoreductase.

SECUTENCE 448 AA; 49586 MW; 0803368EB45024D0 CRC64;
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EMBL; AE016922; AAQ61320.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016491; F:oxidoreductase activity;

GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                        Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082936; PubMed=11214974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                               SEQUENCE FROM N.A. STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=mlr4524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quinol oxidase subunit I
                                                                                                                                                                              Mesorhizobium loti (supplement).";
DNA Res. 7:381-406(2000).
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                                                                                                                                                                                                                                                                  "Complete genome structure of the nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
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(TremBirel. 18, Last sec
(TremBirel. 24, Last and
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    PubMed=11214968;
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100.0%; Pred. No.
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Q7WBI0; 01-OCT-2003 01-OCT-2003

(TrEMBLrel. 25, (TrEMBLrel. 25,

Last sequence update)

Created)

Q7WBI0

PRELIMINARY;

PRT;

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RESULT 15
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Matches 8
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C STRAINERIMD 2210633 / Serotype 03:K6;

STRAINERIMD 2210633 / Serotype 03:K6;

X MEDLINES-22508454; PubMed=12620739;

X MEDLINES-23508454; PubMed=12620739;

X Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagom A., Naima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kim A., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mec distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

Lancet 361:743-749(2003).

R EMBL; Ap005088; BAC62480.1; -.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

RGO; GO:0016491; F:oxidoreductase activity; IEA.

RGO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; Bac Ubq Cox.

R Pfam; PF01654; Bac Ubq Cox; I.
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SEQUENCE
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Q87H28;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot
Takeuchi C., Yamada M., Tabata S.;
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Bacteria; Proteobacteria;
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DNA Res. 7:331-338(2)
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GO:0006118;
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AP003004; BAB51159.1; -.
O:0016020; C:membrane; IEA.
O:0016491; F:oxidoreductase activity;
O:0006118; P:electron transport; IEA.
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RP STQAIN=12822 / ATCC BAA-587;

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RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

RA Chilling Morth T., Colling M., Cromin A., Davis P., Doggett J.,

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RA Chilling Morth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

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RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

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RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

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Best Local Similarity 100.0%; Pred. No. 3.'
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Cytochrome oxidase subunit I.
Name=cioA; Synonyms=qxtA; OrderedLocusNames=BPP1024;
Bordetella parapertussis.
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Alcaligenaceae; Bordetella.
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CIAQFSVAMADDSLWKPLNYQIL 41                 CIAQFSVAMADDSLWKPLNYQIL 27	; Score 41; DB 2; Length ; Pred. No. 1.6e-36; O; Mismatches 0; Inde:	EMBL/GenBank/DDBJ databas  ; 3A359597FF7079EB CRC64	Shevchenko Y., Bout een E.D., Dickson M., utz J., Myers R.M., lus D.E., Schnerch A of more than 15,000 16899-16903 (2002).	Wagner L., Shenmen C.M. Wagner L., Schaefer C.F. uetow K.H., Schaefer C.F. re T., Max S.I., Wang J. Farmer A.A., Rubin G.M., Onaldo M.F., Casavant T. Toshiyuki S., Carninci Peters G.J., Abramson R. 1 Peters G.J., Abramson R. 1 Peters G.J., Abramson R. 2 Peters G.J., Abramson R. 3 Peters G.J., Abramson R. 4 Peters G.J., Lu X., Gi n M., Madan A., Rodrigue	; Craniata; Vertebrata; E ; Catarrhini; Hominidae;	PRT; 349 AA. Created) Last sequence update) Last annotation update)	ALIGNMENTS	Q6LL94 CAG22120 E314_ADEO7 Q775K7 Q775K5 Q9PX47 Q91CK8 AAR89974 AR89974 Q88PM8 Q6C779 Q8CAT8 Q8CAT8
vi i	h 349; els 0; Gaps 0;	•• © .	Eard G.G., C., Butterfield Y.S., L., Schein J.E., full-length human	Schule Bhat Bhat Hsieh ong L. Sche Pran , Mull naratr J., Hu S R.A. S R.A.	Euteleostomi; Homo.	-		Q61194 photobacter Cag22120 photobact P15135 human adeno Q77815 human adeno Q9px47 human adeno Q9px47 human adeno Q9px47 human adeno Q91ck human adeno Aar89974 human ade Q8Bpm8 pseudomonas Q6e779 saprolegnia QBnc94 homo sapien Q8c9j8 mus musculu Q8cat8 mus musculu Q710p2 oryza sativ

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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., wagatsuma M., Shiratori A.,
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RA Murakami K., Yasuda T., Iwayanagi T., wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
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RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
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RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Ohmori Y.,
RA Gundi R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nawakami T., Nomura Y., Ohamoto S.,
RA Okumura K., Nakaima T., Natana M., Hata H., Watanabe M., Komatsu T.,
Nakagawa S., Senoh A., Sasaki M., Jasaki M.,
Takama M., Hata H., Watanabe M., Komatsu T., Nakagawa K.,
RA Mizushima S., Sugano J., Satoh T., Shirai Y., Makagawa K.,
RA Matsumura K., Nayase T., Nakamura Y., Ohamoto J., Sasaki M.,
Nakajara M., Mata H., Nasuho Y., Yamashita R.,
Nakagara
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             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                  Homo sapiens (Human).
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TISSUE=Uterus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLGGEEKFQERVTKHLIPCIAQFSVAMADDSLWKPLNYQIL 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR008938; ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36:40-45(2004).
212; BAC05261.1; -.
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101574 MW;
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Last annotation update)
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Pred. No. 3.5
0; Mismatches
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RESULT
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenho L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenho L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
BOSSK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Mhiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G.,
A Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
A Alakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Schein J.E.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Schein J.E.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Schein J.E.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Schein J.E.,
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Best Local :
  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH65205
AAH65205;
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOWITTER 1 (JAN-2004) to the EMBL; BC065205; AAH65205.1; InterPro; IPR008938; ARM.
                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                   TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RLGGEEKFQERVTKHLIPCIAQFSVAMADDSLWKPLNYQIL
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99:16899-16903 (2002).
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Madan
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SOR RECEIVED
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BP28_HUMAN
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A Cta T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., A Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Wamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., A Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., A Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Ra Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Ra Yujimori K., Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Ra Yugiya S., Mondi F., Hara R., Takeuchi K., Arita M., Hoshida S., Ono Y., Takipuchi S., Watanabe S., Yosida M., Hotuta T., Ra Kusano J., Kanehori K., Takahashi-Pujii A., Hara H., Tanase T.-O., Ra Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Ra Yoshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Ra Yamazaki M., Watanabe K., Kumagai A., Itakuma S., Pukuzumi Y., Ra Yamazaki M., Watanabe K., Kumagai A., Itakuma S., Pukuzumi Y., Ra Cho, Y., Yamada K., Pujii Y., Ozaki K., Hirao M., Ohmori Y., Yamada K., Pujii Y., Ozaki K., Hirao M., Ohmori Y.,
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Best Loc
Matches
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Q9H583; Q9W23;
16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 1
05-JUL-2004 (Rel. 44, 1
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia, Eutheria; Primates;
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch J
                                                                                                                                                                                                                                                                                                                                                                     PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1777-2144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1534-2144 FROM N.A. Cobley V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bougueleret L.,
"A novel BAP28 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BAP28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein BAP28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; S.larity 100.0%; F. Conservative 0;
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28 gene and prote
r WO0100669, 04-J
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annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2; 1
Pred. No. 4.1e-36;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae,
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                                                                                             Suzuki O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                  EMBL; AL136105; CAC15948.1;
EMBL; AK001221; BAA91564.1;
SWISS-2DPAGE; Q9H583; HUMAN
InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
-!- SIMILARITY: Belongs to the BAP28 family.
-!- SIMILARITY: Contains 1 HEAT repeat.
                                                                                                                      SEQUENCE
                                                                                                                                                                                VARIANT
                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                           Polymorphism
REPEAT 2:
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            1 RLGGEEKFQERVTKHLIPCIAQPSVAMADDSLWKPLNYQIL
                                                                         Similarity
                                                                                                                                                                                                                                                                                    PS50077; HEAT_REPEAT;
RLGGEEKFQERVTKHLIPCIAQFSVAMADDSLWKPLNYQIL
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ilarity 100.0%;
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1694
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                                                         Score 41; DB 1; Le
Pred. No. 7.1e-36;
Pred. No. 7.1e-36;
                                                                                                                      /FTId=VAR_010942.
W; D66816EE78D8C9B7 CRC64;
                                                                                                                                                                 FTId=VAR_010941
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                                                            Gaps
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RESULT 6
BP28_MACFA
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Q9GM44;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
01-OCT-2004 (Rel. 45, Last anr
Protein BAP28 (QnpA-17571) (Fr
                                                                                                                                                                           Eukaryota; Metazoa; (Mammalia; Eutheria; Eutheria; Eucropithecinae; Macancel TaxID=9541;
                                                                  Osada N., Hida M., Kusuda J., Tanuma R
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
Submitted (OCT-2000) to the -!- SIMILARITY: Belongs to t -!- SIMILARITY: Contains 1 H
                                                                                                                              TISSUE=Brain;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                        Protein BAP28
Name=BAP28;
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                                                      libraries."
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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 e EMBL/GenBank/DDBJ
the BAP28 family.
HEAT repeat.
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RESULT QRECULT ID VCK1
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

A Hopkins R.F., Jordan H., Moore T., Kasavant T.L., Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Stapleton M., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

A Brownstein M.J., Walek J.A., Gunaratne P.H.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Hulyk S.W.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Blakes S., Worley K.C., Hale S., Garcia A.M., Gajbus R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakes Ly R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakes Ly R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Karywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.T. Mayra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 26
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BC019693 protein
                                                    EMBL;
                                                                                                               Strausberg R.;
                                                                                                                                              rissue=Mammary tumor.
                                                                                                                                                                             STRAIN=mix FVB/N;
                                                                                                                                                                                                                                                                                                  "Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=mix FVB/N;
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Mammalia; Eutheria;
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Name=BC019693;
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01-MAR-2002
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NON TER
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (Mouse)
                           , BC019693; AAH19693
MGI:2384983; BC0196
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                                                                                      (DEC-2001)
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                                                                                                                                                                                                                                                                                            sequences.
                              BC019693.
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Last annotation update)
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Sciurognathi; Muridae;
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Best Local
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                                   MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P. Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muzamatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8CCT5;
Q8CCT5;
01-MAR-2003
                                                                                                                                                                                                                                    Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery genome Res. 10:1617-1630(2000).
                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., S
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Olfactory brain;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase
"Analysis of the mouse transcriptome based on func
60,770 full-length cDNAs.";
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STRALN=C57BL/6J; TISSUE=Olfactory brain;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430400D06 product:hypothetical ARM reps
structure containing protein, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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"Functional annotation o
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420:563-573(2002).
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                           10:1757-1771 (2000)
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SEQUENCE

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RESULT 10
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A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayatsu N., Hiramoto K., Hiraka T., Kasukawa T.,
A Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Karoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Saaski D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Saasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Saasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Saasaki D., Shibata K., Shinagawa A., Takada Y., Tanaka T.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
B Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
B KMEL, AKO32134; BAC27721.1;
                                                                                                                                                       Matches
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Best Local
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Q7XP06;
01-OCT-2003
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                           Gramene;
SEQUENCE
                                                                                                                                                                                                                                                                                                                         Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSJNBb0013J13.14 protein.
Name=OSJNBb0013J13.14;
 Q9N045
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SEQUENCE 40
                                                                                                                                                                                                                                                        "Sequence and analysis of rice chromosome 4.";
Nature 420:316-320(2002).
EMBL; AL662939; CAE03837.3; -.
                                                                                                                                                                                                                                                                                                              Lan L.,
Han B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12447439;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                     CISCUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

X MEDLINE-22388257; PubMed=12477932;

XX MEDLINE-22388257; PubMed=12477932;

XX MEDLINE-22388257; PubMed=12477932;

XX Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altachenko L., Washina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altachenko L., Washina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altachenko L., Washina T.B., Toshiyuki S., Carninci P., Prange C.,

XX Altachenko L., Washina T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Altachenko S., Woorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Altachenko S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Altachenko S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

XX Altachenko S., Worley A.C., Shevchenko Y., Bouffard G.G.,

XX Altachenko M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altachenko S., L., McComman J.W., Green E.D., Dickeon M.C.,

XX Altachenko M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altachenko M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altachenko M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altachenko M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q80VS5;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9N045;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., H
Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto
"Assignment of 118 novel cDNAs of cynomolgus monkey
chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unnamed protein product.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostu
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 275:31-37(2001).
EMBL; AB046087; BAB01669.1; -.
                                                                                                                                                                                                                              and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280VS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9541;
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                                                         TISSUE=Mammary tumor.
                                                                                              STRAIN=mix FVB/N;
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21458551; PubMed=11574149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RVTKHLI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVTKHLI
                                                                                                                                                                                            cDNA sequences.";
l. Acad. Sci. U.S.
(JAN-2003) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                            WAP-TGF alpha model. 7 months
                                                                                                                                                                                            U.S.A. 99:16899-16903(2002)
the EMBL/GenBank/DDBJ databases
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 30;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB4FC0ACC8261DB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cynomolgus monkey brain to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
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                                                                                                                                                                                                                                                         full-length human
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RESULT 12
Q7TMQ4
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wildin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Tuchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                 Query Match
Best Local S
Matches 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
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                                                                                                                                   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC055302; AAH55302.1; -. Hypothetical protein. SEQUENCE 384 AA; 42138 MW; 36E8A26E61ED1C38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7TMQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FVB/N-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                            STRAIN=FVB/N-3;
TISSUE=Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5
                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 SLWKPLN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75
94
                             31
                                                                 Similarity 7; Conserv
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                                SLWKPLN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLWKPLN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AA; 39817 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.A.
                                                                                                                                                                                                                                                                                                                  Sci.
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100.0%; Pred. No.
                                                                                    17.1%; Score 7; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                MMTV-LTR/INT3 model.
                                                                                                                                                                                                                                                                                                                  U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F11AE62B4A00E4A2 CRC64;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 AA
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o. 37;
                                                                                    DB 2;
                                                                                                                                                                                                                                                5 month old mouse. Taken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           month old mouse.
                                                                                                      Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 365;
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                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                     Gaps
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RESULT
Q6IRC5
ID Q6
                                                                                                                     RA Strausberg R.L., Feingold E.A., Grouie L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schapleton M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Tones S. T. Marra M.A.,
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6IRC5;
05-JUL-2004 (TrEMB)
05-JUL-2004 (TrEMB)
05-JUL-2004 (TrEMB)
MGC78790 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilski ..... Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6IRC5
                                                                                                                                                                                                                        Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ
EMBL, BC070973; AAH70973.1; -.
InterPro; IPR001564; NDK.
InterPro; IPR000666; Thiored.
InterPro; IPR006663; Thiored.
InterPro; IPR006663; Thiored.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=MGC78790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                     Redox-active
SEQUENCE 67
                                                                                                     SMART; SM00562; NDK; 3.

PROSITE; PS00626; RCC1_2; UNKNOWN_1.

PROSITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                      Pfam; PF00034; NDK; 3.
Pfam; PF00005; Thioredoxin; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue=Embryo;
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 225:384-391 (2002) .
                                                                     ve center.
625 AA;
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 ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                genomic
                                                                       70243 MW; 1C0947344FDF3DAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  tools
                   17.1%; Score 7;
100.0%; Pred. No.
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Last annotation updat
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   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagner L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625
                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pontius J., Clifton S.W.,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                 databases
                                   Length 625
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A., Schein J.E.,
     0,
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Alischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Alischenko L., Marusina K., Farmer A.A., Rubin G.M., Frange C.,

RX Alischenko L., Marusina K., Bonaldo M.F., Casawant T.L., Scheetz T.E.,

RX Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,

RX Brownstein M.J., Mediun T.B., Toshiyuki S., Carninci P., Frange C.,

RX Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RX Brownstein M.J., McCornan N.A., Malek J.A., Gunaratne P.H.,

RX Brownstein M.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Schez A.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Cay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Cay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Cay L.J., Hulyk S.W.,

RX Richards M. J., Scheman M., Madan A., Rodrigues S., Sanchez A.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RX RYWINSH M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Alones S. J. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
   029993;
029993;
01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S., Strausberg R.;
Submitted (MAY-2004) to the
EMBL; BC070973; AAH70973.1;
Hypothetical protein.
SEQUENCE 625 AA; 70243 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000
and mouse cDNA sequences.";
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH70973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                 211
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                             GEEKFOE 217
                                                                                                                                                                                                                                                                                                                          GEEKFOE 10
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   (TrEMBLrel. 05, (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70243 MW; 1C0947344FDF3DAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%; Score 7; 1 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
Created)
Last sequence update)
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                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 625;
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Matches 7
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MEDLINS=98049343; PLMMed=9389475; DOI=10.1038/37052;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Rlichardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Rlichardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,

Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,

Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,

Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Kaine B.P.,

Shou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,

Utterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,

Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,

Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,

Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR00437; feoB; 1.
TIGRFAMS; TIGR00650; MG442; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0015093; F:ferrous iron transporter activity; IEA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0015684; P:ferrous iron transport; IEA.
InterPro; IPR003373; FeoB.
InterPro; IPR005289; GTP-binding.
InterPro; IPR005289; GTP-DBG.
InterPro; IPR005285; Small_GTP.
Pfam; PF02421; FeoB; 1.
                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 639 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:364-370(1997).
EMBL; AE001089; AAB90987.1;
EPIR; F69280; F69280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q9X1F8; 1MKY.
TIGR; AF0246; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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OrderedLocusNames=AF0246;
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597
                                                                 18
                                                                                                                                       Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00326;
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                                                                 PCIAQFS 24
                                                                                                                                           Conservative
603
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP10BG.
                                                                                                                                                                                                                                                                                  70367 MW; 6B39B71323C981FB CRC64;
                                                                                                                                17.1%; Score 7; DB 2
100.0%; Pred. No. 58;
Live 0; Mismatches
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Search completed: February 1, 2005, 15:31:09
Job time: 72.5556 secs

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Total number of hits satisfying chosen parameters:
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfles1.pep:*
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                                                            US-08-211-202-130
US-08-545-809A-139
US-09-328-352-8089
US-09-732-210-774
US-09-732-210-774
US-09-732-818-59
US-09-248-796A-17764
US-09-370-767-36572
US-09-270-767-36572
US-09-270-767-36572
US-09-270-767-36572
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US-09-270-767-393
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US-09-328-352-931A-17571
US-09-328-352-931A-17571
US-09-134-0101C-2955
US-09-134-011C-2955
US-09-270-767-34433
US-09-270-767-34433
US-09-270-767-34433
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                      Sequence 130, App
Sequence 8089, App
Sequence 8089, App
Sequence 821, Ap
Sequence 821, Ap
Sequence 59, Appl
Sequence 59, Appl
Sequence 36572, A
Sequence 51789, A
Sequence 110, App
Sequence 110, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 105, Ap
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
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US-08-211-202-130
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION TATA:
APPLICATION NUMBER: GB 9120252.3
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: DAVID W. CLOUGH
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELLEDHONE: 312-474-6300
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GENERAL INFORMATION:
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APPLICANT: BAIER, Michael
APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Chicago
STATE: Illinois
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US-09-889-738-21
US-09-711-870-26
US-09-252-991A-26186
US-09-270-767-43201
US-09-252-991A-18877
US-09-252-991A-18877
US-09-418-963-2
US-09-418-963-2
US-09-252-991A-19290
US-09-252-991A-19290
US-09-252-991A-19290
US-09-252-991A-19290
US-09-252-991A-19290
US-09-252-991A-19290
US-09-253-991A-1920
US-09-543-681A-7870
US-09-543-6801
US-09-346-650-1
US-09-457-040B-27
US-09-457-040B-27
US-09-370-700-6
US-09-370-700-6
US-09-603-207-6
                                             28111/31960
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Result No.

Score

Query Match

Length

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SUMMARIES

Pred. No. is the number of a score greater than or equal and is derived by analysis of

Minimum Maximum

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Beq

length: 21 length: 2000000000

Word size Searched:

0

Sequence: Title: Perfect score:

SEQ5\_2030\_2070

Sequence Sequence

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21, Appl
26186, Appl
26187, A
43201, A
26097, A
26097, A
27097, A
2717, Appl
172, Appl
173, Appl
174, Appl
175, Appl
176, Appl
177, Appl

Sequence Sequence

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Scoring table:

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Gapop 60.0 , Gapext 60.0

Run on: OM protein -

protein search, using sw model

Copyright

Database :

Issued\_Patents\_AA:\*

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Post-processing: Listing first 45 summaries

TELEFAX:

312-474-0448

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Matches
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amin
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                                                           Matches
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/.
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 1
FILING DATE: 27-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Pumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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CITY: Boston
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y Match 17.1%; Score 7; DB Local Similarity 100.0%; Pred. No. 1. hes 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 06
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                                                                                                                                                                                                                                           TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
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amino acid
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                             KFQERVT 13
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                                                                                                                                    protein
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                                                        17.1%; Score 7; DB : 100.0%; Pred, No. 1.0 tive 0; Mismatches
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                                                                        DB 3;
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RESULT 3

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US-09-543-681A-8221

Sequence 8221, Application US/09543681A

Sequence 8221, Application US/09543681A

Patent NO. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 774
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Best Local Similarity
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Patent No. 6562958
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wu, Yonnie S. TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use FILE REFERENCE: 38-21 (15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bunkers, Greg J. APPLICANT: Liang, Jihong APPLICANT: Mittanck, Cindy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Micrococcus luteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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6, Conserv
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Pred. No.
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-59
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US-09-370-838-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-248-796A-17764
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TYPE: PRT

ORGANISM: Proteus mirabilis
US-09-543-681A-8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17764
LENGTH: 123
                                                                                                               NUMBER OF SEQ ID NOS: 289
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 125
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No. 6444425
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SEQ ID NO 8221
LENGTH: 123
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Best Local Similarity
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Query Match
Best Local Similarity
                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Reather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EXALIER FILING DATE: 1999-04-02
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100.0%; Pred. No. 23;
tive 0; Mismatches
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100.0%; Pred. No. 23
tive 0; Mismatches
  14.6%; Score 6; DB 4; 100.0%; Pred. No. 24;
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                  Length 125;
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RESULT 10
US-09-270-767-36572
; Sequence 36572, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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Best Local Similarity
Tatches 6; Conserv
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                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-7848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-7848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapien US-09-854-133-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 125
                                                                                                                                                                                                                                                                                                  APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2700-01-27
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7848
LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7848, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
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Patent No. 6759508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 6; Conserv
                                                                                                                     104 LWKPLN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43
                                                                                                                                                    32 LWKPLN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 IAOFSV 48
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100.0%; Pred. No. 26;
tive 0; Mismatches
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%; Pred. No. 24;
0; Mismatches
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Best Local Similarity
""" hes 6; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 20842
                                                                                                                                                                                                                                                                                                                                           Sequence 20842, Ap
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Best Local :
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51789
LENGTH: 145
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767 CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 NORTH SEQ ID NOS: 62517 NORTH SECTIONALE: Patentin Ver. 2.0
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa means any amino acid
                                          ENGTH: 149
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                                                                                                                                                                                                                                                                                                                       INFORMATION:
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APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Bougueleret, Lydie
TITLE OF INVESTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: U9/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-02-19
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-08-10
FEALLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER: OF SEQ ID NOS: 182
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Best Local Similarity
"hes 6; Conserv:
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                             Sequence 466, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patent.pm
SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 110, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                            CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
                                                                                                 EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
                                                                                  EARLIER
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/149,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                 APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07 APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 PLNYQI
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100.0%; Pred. No. 29;
60/040,334
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R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,633
R APPLICATION NUMBER: 60/047,633

APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600

FILING DATE: 1997-05-23

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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
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APPLICATION NUMBER: 60/056,887
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APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
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APPLICATION NUMBER: 60/040,162
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APPLICATION NUMBER: 60/056,884
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APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/043,672
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APPLICATION NUMBER: 60/043,314
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ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,631
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,845
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,892
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/047,595
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ER FILLING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER FILLING DATE: 1997-06-23
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APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
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APPLICATION NUMBER: 60/056,872
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APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER: 60/056,630
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APPLICATION NUMBER: 60/056,894
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ER FILING DATE: 1997-08-22
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ER APPLICATION NUMBER: 60/049,610
ER FILING DATE: 1997-06-13
ER APPLICATION NUMBER: 60/061,060
ER FILING DATE: 1997-10-02
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ER APPLICATION NUMBER: 60/056,881
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,909
ER FILING DATE: 1997-08-22
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ER FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22
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                                                           Similarity 100 6; Conservative
PLNYOI
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                                                                         14.6%;
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o. 29;
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Search completed: February 1, 2005, 15:35:47 Job time : 18.5556 secs

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Maximum DB seq length: 2000000000
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Perfect score:
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Published Applications AA:*

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2: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1.3	12	11	10	9	8	7	6	5	4	w	2	_	Result No.
7	7	7	7	7	7	7	7	7	7	89	8	41	Score
17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	19.5	19.5	100.0	Query Match 1
238	98	98	98	98	98	98	98	98	36	188	132	1149	Query Match Length DB
16	16	15	15	15	5	15	14	14	9	15	15	17	E
US-10-767-701-41775	US-10-379-392-8	US-10-029-926B-38	US-10-453-698-48	US-10-032-423A-38	US-10-029-988B-38	US-10-032-037B-38	US-10-308-817-48	US-10-194-975-8	US-09-864-761-44493	US-10-424-599-199301	US-10-424-599-200002	US-10-128-558-167	ID
Sequence 41775, A	Sequence 8, Appli	Sequence 38, Appl	Sequence 48, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 48, Appl	Sequence 8, Appli	Sequence 44493, A	Sequence 199301,	Sequence 200002,	Sequence 167, App	Description

### ALIGNMENTS

RESULT 1

NUMBER OF SEQ ID NOS: 412

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SEQ ID NO 167

LENGTH: 1149

TYPE: PRT

ORGANISM: Homo Bapiens

US-10-128-558-167
                                      ; OTHER INFORMATION: Clone ID: US-10-424-599-199301
                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-199301
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 199301, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200002
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Query Match
                                                                                                                                SEQ ID NO 199301
LENGTH: 188
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_22628C.1.pep-10-424-599-200002
                                                                                                                                                                   APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FULL REFERENCE: 38-21(53223)B
FULL REFERENCE: US/10/424,599
FULL REFERENCE: 203-04-28
                                                                                                                                                                                                                                                                                                  APPLICANT: La ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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                                                                         TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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ORGANISM: Glycine max
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                                                    PAT_MRT3847_21993C.1.pep
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   Score 8;
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Pred. No. 5.4e-36;
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b. 0.96;
   DB 15;
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   Length 188;
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                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
SEQ ID NO 44493
LENGTH: 36
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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APPLICANT: Chen, Wensheng
RITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30
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OTHER
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                                                                                           OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                    TYPE: PRT
                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00665
                                  R INFORMATION:
R INFORMATION:
R INFORMATION:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G DATE: 2001-01-30
CATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                       CATION NUMBER: US 60/234,687
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                                : MAP TO AC005229.1
: EXPRESSED IN PLACE:
: EXPRESSED IN FETAL
: EXPRESSED IN BRAIN
: EXPRESSED IN LUNG,
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                                FETAL LIVER, SIGNAL
BRAIN, SIGNAL = 0.86
LUNG, SIGNAL = 1
BONE MARROW, SIGNAL = 1.1
ADULT LIVER, SIGNAL = 0.86
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Sequence 48, Application US/10308817

Publication No. US20030219861A1

GENERAL INFORMATION:

APPLICANT: Rother, Russell

APPLICANT: Wu, Dayang

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 1087-37

CURRENT APPLICATION NUMBER: US/10/308,817

CURRENT FILING DATE: 2002-12-03

NUMBER OF SEQ ID NOS: 195

SOFTWARE: PatentIn version 3.1

SEQ ID NO 48

LENGTH: 98

TYPE: PRT

ORGANISM: human

US-10-308-817-48
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-8
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                                                                                          RESULT 7
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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10194975
publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
Sequence 38, Application US/10032037B
Publication No. US20040001822A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
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Best Local Similarity
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Best Local (
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100.0%; Pred. No. 3.8;
tive 0; Mismatches
                                                                                                                                                                                                                17.1%; Score 7; DB 14; Length 98; 100.0%; Pred. No. 9.2; tive 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-029-988B-38
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Best Local Similarity
7; Conserve
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US-10-032-423A-38
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US-10-029-988B-38
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                                                    Sequence 38, Application US/10032423A

Publication No. US20040002450A1

Publication No. US20040002450A1

GENERAL IMFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/45

CURRENT APPLICATION NUMBER: US/10/032,423A

CURRENT APPLICATION NUMBER: 60/258,948

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR APPLICATION NUMBER: 12/29/2000

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 38
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CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FASESEQ for Windows Version 3.0

SEQ ID NO 38

LENGTH: 98

TENGTH: 98
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Best Local Similarity
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CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y.17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46
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TYPE: PRT
                 LENGTH: 98
TYPE: PRT
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ORGANISM: Homo sapiens
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100.0%; Pred. No.
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100.0%; Pred. No.
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Sequence 38, Application US/100299268

| Sequence 38, Application US/100299268
| Publication No. US20040073011A1
| GENERAL INFORMATION:
| APPLICANT: HAGAY, et al.
| APPLICANT: HAGAY, et al.
| TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY FILE REFERENCE: 10793/50
| CURRENT FILING DATE: 2001-12-31
| PRIOR APPLICATION NUMBER: 60/258,948
| PRIOR APPLICATION NUMBER: 60/258,948
| PRIOR PILING DATE: 12/29/2000
| NUMBER OF SEQ ID NOS: 203
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 38
| LENGTH: 98
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-10-029-926B-38
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; Publication No. US20040038308A1
; GENERAL INFORMATION;
APPLICANT: Rother, Russell
: TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION UNWHER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-453-698-48
                                                                            RESULT 12
US-10-379-392-8
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US-10-029-926B-38
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US-10-453-698-48
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                  Sequence 8, Application US/10379392 Publication No. US20040110226A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                   Query Match 17.1%; Score 7; DB 15; Best Local Similarity 100.0%; Pred. No. 9.2; Matches 7; Conservative 0; Mismatches
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Gregory Alan
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RESULT 14
US-10-112-944-472
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US-10-767-701-41775
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; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 41775
LENGTH: 238
                                                                                                                                                                                           Sequence 472, Application US/10112944
Publication No. US20040048249A1
                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41775, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
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Matches 7; Conserv
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Best Local
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                                                                                                                                   APPLICANT: Tang, Y. Tom APPLICANT: Yang, Yongh
                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                         211 LGGEEKF 217
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                                     Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
Wang, Jian-Rui
Wehrman, Tom
Ghosh, Malabika
                                                                                                                Yang, Yonghong
Weng, Gezhi
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Pred. No.
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FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-28
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-11
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2000-05-18
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SOFTWARE: pt FL_genes Version 5.0
SEQ ID NO 472
LENGTH: 600
TYPE: PRT
ORGANIZM: Homo sapiens
US-10-112-944-472
                                                                           Query Match 14.6%; Score 6; DB 17; Length 47; Best Local Similarity 100.0%; Pred. No. 60; Matches 6; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
26 FÇERVT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 KFQERVT 13
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Search completed: February 1, 2005, 15:44:53 Job time : 60.7778 secs

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Post-processing: Listing first 45 summaries
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length: 2000000000
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154.882 Million cell updates/sec
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                                        US-09-489-039A-7912
US-09-489-039A-9854
US-09-489-039A-9854
US-09-543-681A-4532
US-09-543-681A-20403
US-09-262-991A-20403
US-08-714-741-46
US-08-714-741-41
US-09-68-714-741-41
US-09-68-714-741-41
US-09-68-13-996C-4343
US-09-68-13-976-5794
US-09-134-001C-3670
US-09-134-001C-3670
US-09-134-001C-3670
US-09-134-001C-3670
US-09-134-001C-3670
US-09-136-657-3
US-09-136-657-3
US-09-136-657-3
US-09-138-352-6245
US-09-38-352-6245
-08-723-142A-18
-09-528-784A-18
-09-569-098A-18
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                                        4343, Ap
57083, Ap
57084, Ap
41841, A
670, Appli
3670, Appli
3, Appli
1, Appli
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6481, Ap
9854, Ap
4532, Ap
20403, A
3, Appli
42, Appl
46, Appl
                                                                                                                                                                                                                                                      41, Appl
              App]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 7912

LENGTH: 411

TYPE: PRT

ORGANISM: Klebsiella pneumoniae
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                             US-09-543-681A-6481
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US-09-543-681A-6481
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GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: GARY Breton et. al
TITLE OF INVENTION: HUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
                                                                                 GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7912, Application Patent No. 6610836
                                                                                                                                                                                                                                                       Sequence 6481, Application US/09543681A Patent No. 6605709
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Best Local Similarity
Query Match
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                                       LENGTH: 457
TYPE: PRT
ORGANISM: Proteus mirabilis
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US-08-990-571-28
US-08-723-142A-28
US-09-528-784A-28
US-09-528-784A-46
US-08-945-258-46
US-08-9528-784A-46
US-08-9528-784A-46
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Pred. No.
 Score 8;
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DB 4; ). 0.49;

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Query Match

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US-09-252-991A-20403
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                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4532
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US-09-543-681A-4532
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Best Local Similarity
Matches 8; Conserve
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Matches 8
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US-09-489-039A-9854
                                    Sequence 20403, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4552
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GARY BRETON
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LENGTH: 473
         APPLICANT: Marc J.
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gary Br
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CURRENT APPLICATION NUMBER: US/09/489,03:
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                              139 LTAFFLEA 146
                                                                                                                                                                                             34 LTAFFLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4532, Application US/09543681A
o. 6605709
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                                                                                                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                               Conservative
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Rubenfield et al. NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                        19.5%; but
100.0%; Pr
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o. 0.55;
                                                                                                                                                                                                                                                              Length 480;
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Best Local Similarity
Marches 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptococcus pneumoniae US-09-286-981B-3
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US-09-286-981B-3
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SEQ ID NO 3
LENGTH: 431
TYPE: PRT
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                                                                                                                                                                                                                                            Sequence 42,
Patent No. 69
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20403
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CURRENT FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: US 60/085,743
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Johnson, Leslie S
TITUE OF INVENTION: Derivatives of Choline
FILE REFERENCE: 469201-396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wizemann, The APPLICANT: Koenig, Scott APPLICANT: Johnson, Lesl
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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APPLICANT: Yother, Janet
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES
TITLE OF INVENTION: PORTIONS AND PRODUCTS
TITLE OF SEQUENCES: 47
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                              Application US/08714741
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                                                                                                                                                      Briles, David E. McDaniel, Larry S Swiatlo, Edwin Yother, Janet
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Pred. No.
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ADDRESSEE:

Curtis, Morris & Safford, P.C.

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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
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APPLICANT:
APPLICANT:
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/714,741 FILING DATE: 16-SEP-1996
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
NUMBER OF SEQUENCES: 47
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 100.0%; Pred. No.
hes 7; Conservative 0; Mismatch
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: New York
STATE: New York
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                              COUNTRY: U.S.
ZIP: 10036
                                                                                                                                                                                                 CITY: New York
STATE: New York
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CLASSIFICATION:
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Swiatlo, Edwin
Yother, Janet
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Hollingshead, Susan
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o. 8.6;
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MOLECULE TYPE: US-08-714-741-40
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Best Local
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                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Ve.
CURRENT APPLICATION UNMBER: US/08/714,741
APPLICATION UNMBER: US/08/714,741
FILING DATE: 16-SEP-196
CLASSIFICATION: 435
                                                                             TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO: 4
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 605 amino acide
TYPE: amino acid
TYPE: amino acid
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                 NAME: Frommer Esq., William S. REGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 45431 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
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APPLICANT:
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STATE: New York
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TOPOLOGY: li
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                                  TOPOLOGY:
                                              STRANDEDNESS:
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                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      530 Fifth Avenue
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Brooks-Walter, Alexis
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              amino acid
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b; Pred. No. 8.8
0; Mismatches
                                                                                                                                                                                       454312-2460
                                                                                                                                                                                                                                                                                                                                 Version #1.30
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RESULT 11
US-09-513-999C-4343
; Sequence 4343, Application US/09513999C
; Patent No. 678961
; GENERAL INFORMATION:
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Best Local S
Matches 7
                                                                                                                                                                 Matches
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                           TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: Brooks WA
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                              NAME: Frommer Esq., william S. REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
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New York

New York

New York

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Swiatlo, Edwin
"--her, Janet
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VENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,

VENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
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Crain, Marilyn J.
Hollingshead, Susan
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Pred. No.
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o. 17;
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o. 12;
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FEQUENCE 5794, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

ITILE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
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Best Local Similarity
Matches 6; Conserva
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US-09-621-976-5794
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Best Local Similarity
Watches 6; Conserve
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 57083

LENGTH: 56

TYPE: PRT
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GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4343
LENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: score 5.4
OTHER INFORMATION: seq LLCYPGWSAVAQS/QL
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ORGANISM: Homo sapiens
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100.0%; Pred. No.
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o. 14;
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Sequence 41841, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41841
LENGTH: 142
TYPE: PAT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41841
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -53..-1
US-09-621-976-5794
                                                                                                                                                           Sequence 6, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO
SEQ ID NO
SEQ ID NOS: 6849
SEQ ID NO
SEQ ID NOS: 6849
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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US-09-198-452A-6
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US-09-270-767-41841
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Best Local Similarity 100.0%; Pred. No. 32,
Matches 6; Conservative 0; Mismatches
                                                                              Query Match 14.6%; Score 6; DB 4; Best Local Similarity 100.0%; Pred. No. 32; Matches 6; Conservative 0; Mismatches
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LENGTH: 97
                                  13 SILQEH 18
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75 SILQEH 80
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Search completed: February 1, 2005, 15:35:43 Job time : 18.5556 secs



Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Minimum |
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DB seq length: 2000000000
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### SUMMARIES

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US-09-748-875-63 US-09-298-523B-63	US-10-299-636-95	US-09-748-875-14 US-09-298-523B-14	US-09-748-875-4 US-09-298-523B-4	US-10-254-995-3	US-10-282-122A-68101	US-10-128-558-167	ID
Sequence 63, Appl Sequence 63, Appl	Sequence 97, Appl Sequence 95, Appl	Sequence 14, Appl Sequence 14, Appl	Sequence 4, Appli Sequence 4, Appli	Sequence 103, Appli Sequence 3, Appli	Sequence 68101, A	Sequence 167, App	Description

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US-10-767-701-61193	US-10-424-599-204559	424-599-	7	-599-	-115	US-10-425-115-261981	US-10-029-386-29893	US-10-425-115-191450	-10-425-115-29968	-10-425-115-21028	US-10-425-115-356680	US-10-425-115-216216	US-10-227-577-1049	091-504-104	US-09-764-891-5371	US-09-764-869-1049	US-10-437-963-136574	US-10-299-636-94	US-09-298-523B-60	US-09-748-875-60	US-10-291-265-459	US-09-298-523B-3	48-8	US-09-298-523B-2	US-09-748-875-2	US-09-298-523B-62	US-09-748-875-62	US-09-298-523B-1	US-09-748-875-1	US-09-298-523B-61
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### ALIGNMENTS

US-10-128-558-167

| Sequence 167, Application US/1012858|
| Publication No. US20040219521A1|
| GENERAL INFORMATION:
| APPLICANT: Tang, X. Tom
| APPLICANT: Wang, Zhiwei
| APPLICANT: Wang, Zhiwei
| APPLICANT: Boyle, Bryan J
| APPLICANT: Drmanac, Radoje T
| TITLE OF INVENTION: NOVel Nucleic Acids and
| TITLE APPLICATION NUMBER: US/10/128,558
| CURRENT FILING DATE: 2001-12-11
| PRIOR APPLICATION NUMBER: US 60/339,453
| PRIOR APPLICATION NUMBER: US 60/339,453
| PRIOR APPLICATION NUMBER: US 99/488,725
| PRIOR APPLICATION NUMBER: US 99/552,317
| PRIOR APPLICATION NUMBER: US 99/552,317
| PRIOR APPLICATION NUMBER: PCT/US00/35017
| PRIOR APPLICATION NUMBER: PCT/US00/35017
| PRIOR APPLICATION NUMBER: US 99/491,404
| PRIOR APPLICATION NUMBER: US 99/491,404
| PRIOR APPLICATION NUMBER: US 99/496,914
| PRIOR APPLICATIO

NUMBER OF SEQ ID NOS: 412 SOFTWARE: pt\_FL\_genes Version 6.0 SEQ ID NO 167

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US-10-128-558-167

TYPE: PRT ORGANISM: Homo sapiens

ENGTH:

1149

Query Match 48.8%; Score 20; Best Local Similarity 100.0%; Pred. No. Matches 20; Conservative 0; Mismatch

0; Mismatches

DB 17; 8.2e-13;

Length 1149;

Indels

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Gaps

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RESULT 2 US-10-282-122A-70087

ence 70087, Application US/10282122A ication No. US20040029129A1

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US-10-282-122A-70087
                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 70087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
                                                                                                                                    ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/230,335
34 LTAFFLEA 41
                                                                                                                                                                                                                                                                                         ING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                     ICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                     CATION NUMBER: 60/267,636
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                                                   Conservative
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                                                                 19.5%; Score 8; 1
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                                                     Mismatches
                                                                     DB 15;
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                                                                                    Length 443;
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                                                      0;
                                                      Gaps
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Yother, Janet Crain, Marilyn J Hollingshead, Susan McDaniel, Larry Swiatlo, Edwin

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RESULT
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US-10-299-636-103
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                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Pate:
SEQ ID NO 68101
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Best Local Similarity
                 GENERAL INFORMATION:
                                Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/207,727
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APPLICANT: Briles, David E
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas putida
                                                                                                                                                                                                                                                                                                                             LENGTH: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/242,578
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                                                   103,
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Yamamoto, Robert
Forsyth, R.
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                                   Application US/10299636
o. US20040077847A1
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Pred. No.
                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                               Length 467;
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FITLE OF INVENTION: Identification of Essential Genes in Microorganisms

Carr, Grant Yamamoto, Robert Foreyth, R.

Trawick

Daniel t, John

Ohlsen, Kari Zyskind, Judith

Zamudio, Carlo Malone, Chery Haselbeck, Robert

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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-10-254-995-3
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-10-299-636-103
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Sequence 4, Application US/09748875
Publication No. US20010016200A1
GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
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Best Local Similarity
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Publication No. US20030138447A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Wizemann, Leslie S
APPLICANT: Wizemann, Leslie S
ITILE ORI INVENTION: Derivatives of Choline Binding Proteins for Vaccines
FILE REFERENCE: 469201-396
CURRENT APPLICATION NUMBER: US/10/254,995
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/99/286,981
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
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TITIE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
FILE REFERENCE: 57908/361
CURRENT APPLICATION NUMBER: US/10/299,636
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 08/714,741
PRIOR FILING DATE: 1996-09-16
PRIOR APPLICATION NUMBER: 08/529,055
PRIOR APPLICATION NUMBER: 08/529,055
PRIOR APPLICATION NUMBER: 08/529,055
PRIOR FILING DATE: 1995-09-15
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PALCANTON Ver: 2.1
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Local Similarity 100.0%; Pred. No. 31,
es 7; Conservative 0; Mismatches
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100.0%; Pred. No.
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; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PAT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-4
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Best Local Similarity
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US-09-298-523B-4
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                                                                                                                              ; ORGANISM: Streptococcus pneumoniae US-09-748-875-14
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US-09-748-875-14
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                                                                                                                                                                                                                                      Sequence 14, Application US/09748875

Publication No. US20010016200A1

GENERAL INFORMATION:

APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERENCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 09/298,523

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23
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TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/298,523B
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09298523B Publication No. US20030059438A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 496
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                              TYPE: PRT
                                                                                                                                                                            LENGTH:
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324 KKEELTS 330
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                              KKEELTS 29
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                                                                            17.1%; Score 7;
100.0%; Pred. No.
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0; Mismatches
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US-10-299-636-95
Sequence 95, Application US/10299636
Publication No. US20040077847A1
GENERAL INFORMATION:
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                                                                        RESULT 11
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SEQ ID NO 14
LENGTH: 589
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SEQ ID NO 97
LENGTH: 589
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Best Local
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Publication No. US20030059438A1
GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
ETT DEFENCE: AFAIRM AND STRAINS THEREOF AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97, Application US/10299636 Publication No. US20040077847A1
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Best Local (
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PRIOR FILING DATE: 1995-09-15
NUMBER OF SEQ ID NOS: 111
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/714,741
PRIOR FILING DATE: 1996-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/299,636
CURRENT FILING DATE: 2002-11-19
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CURRENT FILING DATE: 1999-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tart, Rebecca
APPLICANT: Brooks Walter, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT: McDaniel, Larry
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                                                                                                                                                                                                              Local
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Crain, Marilyn J
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Swiatlo, Edwin
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100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No.
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US-09-748-875-63
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Best Local Similarity
'arches 7; Conserve
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                                                                                   Sequence 63, Application US/09298523B Publication No. US20030059438A1 GENERAL INFORMATION:
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SEQ ID NO 63
LENGTH: 670
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Best Local :
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APPLICANT: BRILES et al.
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           APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERENCE: 454312-3140 CURRENT APPLICATION NUMBER: US/09/748,875 CURRENT FILING DATE: 2000-12-26 PRIOR APPLICATION NUMBER: 09/298,523 PRIOR FILING DATE: 1999-04-23 NUMBER OF SEQ ID NOS: 78
CURRENT APPLICATION NUMBER: US/09/298,523B
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PRIOR APPLICATION NUMBER: 08/714,741
PRIOR FILING DATE: 1996-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 64
TYPE: PRT
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PRIOR FILING DATE: 1995-09-15
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
FILE REFERENCE: 57909/361
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Swiatlo, Edwin
Swiatlo, Janet
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Tart, Rebecca
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Crain, Marilyn J
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100.0%; Pred. No.
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RESULT 15
US-09-298-523B-61
; Sequence 61, Application US/09298523B
; Dublication No. US20030059438A1
; Publication No. US20030059438A1
; GENERAL INFORMATION:
APPLICATI REILES et al.
APPLICATI INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
; CURRENT FILING DATE: 1999-04-23
; CURRENT FILING DATE: 1999-04-23
; CURRENT FILING DATE: 1999-04-23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 61
; SEQ ID NO 61
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
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US-09-748-875-61

US-09-748-875-61

Sequence 61, Application US/09748875

Publication No. US20010016200A1

GENERAL INFORMATION:
APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140

CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOPTWARE: PATENTIN Ver. 2.1
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NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 63

LENGTH: 670

TYPE: PRT

ORGANISM: Streptococcus pneumoniae
US-09-298-523B-63
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-61
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Best Local 9
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Local Similarity 100.0%; Pred. No. 56,
hes 7; Conservative 0; Mismatches
                                                             y Match 17.1%; Score 7; DB 10; Length 690; Local Similarity 100.0%; Pred. No. 58; hes 7; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 58;
hes 7; Conservative 0; Mismatches
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23 KKEELTS 29
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5.56;
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Db 361 KKEELTS 367

Search completed: February 1, 2005, 15:44:48 Job time: 60.7778 secs

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Minimum
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## ALIGNMENTS

C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_charc: 0;Accession: AG0546

09-Nov-2001 #text\_change 18-Nov-2002

Salmonella enterica subsp. enterica serov

probable terminal oxidase chain I [imported] - C;Species: Salmonella enterios anterios

#### R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUID:21534947; PMID:11677608 A; Accession: AG0546 A;Cross-references: UNIPROT:007440; EMBL:Y10528; NID:g2208963; PIDN:CAA71555.1; A;Experimental source: strain PAO1, substrain PAO6049 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J.DY, S.; Olson, M.V. Nature 406, 959-964, 2000 R;Cunningham, L.; Pitt, M.; Williams, H.D. Mol. Microbiol. 24, 579-591, 1997 Mol. Microbiol. 24, 579-591, 1997 A;Title: The cioAB genes from Pseudomonas aeruginosa code for a A;Reference number: 224440; MUID:97323403; PMID:9179851 A;Accession: T47273 cyanide insensitive terminal oxidase chain cioA [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004 C;Accession: T47273; G83155 밁 5 A;Gene: STY0392 C;Superfamily: cytochrome d complex terminal oxidase chain A,Status: preliminary A,Molecule type: DNA A,Residues: 1-467 <PAR> A,Cross-references: GB:AL513382; PIDN:CAD08815.1; PID:g16501629; A; Molecule type: DNA A; Residues: 1-488 <CUN> A;Status: preliminary; translated from GB/EMBL/DDBJ Query Match Matches N Local 102 LTAFFLEA 109 34 LTAFFLEA 41 Similarity Conservative G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, 19.5%; Score 8; 1 100.0%; Pred. No. tive 0; Mismatc Mismatches DB 2; o. 0.79; 0; Length 467; Indels novel cyanide-insensitiv GSPDB:GN00176 ٥. Gaps 0 M.J.; Br K.; Lim, PID: 9220

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, and Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g17780 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84556
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A;Molecule type: DNA
A;Residues: 1-488 <STO>
A;Cross-references: GB:AE004810; GB:AE004091; NID:g9950106; PIDN:AAG07317.1; GSPDB:GN001
                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-417 <STO>
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A;Accession: D84556
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A;Molecule type: DNA
A;Residues: 1-276 <WAT>
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A; Introns: 137/3
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83155
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                                                                                                                                          Cross-references: GB:AE002093; NID:g6598810; PIDN:AAB80787.2; GSPDB:GN00139;
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17.1%; Score 7; DB 2;
100.0%; Pred. No. 8.4;
tive 0; Mismatches
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100.0%; Pred. No. 5.8;
Live 0; Mismatches
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A; Introns: 33/3; 66/3; 261/2; 299/3; 479/2; 615/3; 750/3; 903/2; C; Superfamily: Caenorhabditis elegans F44B9.6 protein
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C;Genetics:
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Matches 7; Conserve
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                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-960 < ANT>
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J. Bacteriol. 173, 6230-6241, 1991
A;Title: Cloning, characterization, and expression in Escherichia coli of the genes encor A;Reference number: A38170; MUID:92011387; PMID:1655703
A;Accession: A38170
                                                                                                                                                                                                                                                                                A; Status: preliminary
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A;Molecule type: DNA
A;Residuss: 1-13 <-MO2>
A;Cross-references: GB:M77787
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A;Molecule type: DNA
A;Residues: 1-537 <MOS>
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the C. elegans cosmid F44B9
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hypothetical protein F28B23.2 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: H86389 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
photosystem I chain IX - Cyanophora paradoxa cyanelle C;Species: cyanelle Cyanophora paradoxa C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C;Accession: T06840 R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryan's submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:021237; EMBL:AF007261; NID:g2258325; PIDN:AAD11864.1; A;Experimental source: ATCC 50394 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997
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C; Keywords: mitochondrion;
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R;Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, Nature 387, 493-497, 1997
Nature 387, 493-497, 1997
A;Title: An ancestral mitochondrial DNA resembling a eubacterial A;Reference number: S78127; MUID:97311393; PMID:9168110
A;Accession: S78131
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A;Residues: 1-1196 <STO>
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Best Local
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larity 100.0%; Pred. No. 21
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100.0%; Pred. No.
tive 0; Mismatc
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-75 < KAN>
                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence
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Similarity 6; Conserv

14.6%; ilarity 100.0%; Conservative

Score 6; DB 2; Pred. No. 22; 0; Mismatches

DB 22;

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Length 75;

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RESULT 10
S04666
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75054
C;Accessio
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J. Mol. Biol. 179, 185-214, 1994
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04666
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C;Superfamily: photosystem I protein psaJ
C;Keywords: cyanelle; photosynthesis; photosystem
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A;Accession: T06940
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-40 <STI>
                                                                                                                                                                                                                                        C; Species: Synechocystis sp. A; Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                    hypothetical protein ssl3127 -
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A; Residues: 1-69 < TYB>
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100.0%; Pred. No.
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hypothetical protein DKFZp434M0326.1 - C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision C;Accession: T46439
                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:P73195; EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAA1722 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: ferredoxin [2Fe-25], Clostridium type C;Keywords: 2Fe-25; electron transfer; iron-sulfur protein; metalloprotein F;32,40,80,84/Binding site: 2Fe-25 cluster (Cys) (covalent) #status predicted
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75307
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C;Superfamily: Thioredoxin; thioredoxin homology
C;Kupwords: hear-stable protein; redox-active disulfide
F;10-93/Domain: thioredoxin homology <THR>
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                                                                                            T46439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-107 <JOH>
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                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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;Species: Chromatium vinosum
;Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
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                        #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
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Search completed: February Job time: 15.5556 secs

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A;Molecule type: mRNA
A;Residues: 1-137 <AAA>
A;Cross-references: UNIPROT:Q9NSX2; EMBL:AL137681
A;Experimental source: adult testis; clone DKFZp4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ansorge, W.; Wirkner, U. submitted to the Protein St A;Reference number: Z23028
                                                                                                                                                                                                                                                                R;Shirai, M.; Hirakawa, H.; Kimoto, M.;
Nucleic Acids Res. 28, 2311-2314, 2009
A;Title: Comparison of whole genome sequence of the comparison of whole sequence number: A86491; MUID:2033034
A;Accession: B86624
                                                                                                                                                                                                                                                                                                                                                                     HTH transcription regulator [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A;Experimental source: strain J138
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s; Pred. No. 38;
0; Mismatches
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# SUMMARIES

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Aab41161	Aay57954	Aau91137	Abr01787	Abb54604	Aau91087	Aag57341	Ad105626	Aam25936	Aau91110	Aab14126	Aag00535	Aay65259	Abp79600	Aau32861	Adh62559	Aae25974	Aar32985	Aag19461	Abu20127
L Human ORF	Human tra	7 Human sec	1 Human bre	Lactococc		L Arabidops	M. catarr	6 Human pro	) Human sec	6 Bordetell	Human sec		N. gonorr	Novel hum	) Cardiac m	Human pro	Encoded b		_

ALIGNMENTS

#### RESULT 1 ADE08012 CCCCX88X7777X882717X8X8888888888X88X88X88X81X8AXX Unidentified. novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder. Novel protein (useful for identifying genetic disorders) #167. ADE08012; ADE08012 standard; protein; 1149 AA. 03-JUL-2003. 29-JAN-2004 WO2003054152-A2 (first entry)

10-DEC-2001; 11-DEC-2001; 14-MAR-2002; 14-MAR-2002; 12-APR-2002; 12-APR-2002; 12-APR-2002; 22-APR-2002; 10-DEC-2002; 2002WO-US039555 24-APR-2002; 2002US-0365384P. 2002US-0372381P. 2002US-0372615P. 2002US-00128558. 2002US-0376045P. 2001US-0339739P. 2001US-0339453P. 2002US-0365091P.

(HYSE-) HYSEQ INC.

Tang YT, Asundi V, Goodrich RW, Ren F, Zhang Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Ma Y, Wang D, Chen R, Xu C, Boyle BJ; J, Zhao QA, Drmanac RT, Wang J; Wang Z;

N-PSDB; ADE07101. WPI; 2003-569235/53.

New polymucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.

Claim 20; SEQ ID NO 1078; 1177pp; English.

The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially

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Conservative

100.0%;

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The sequence is that of a protein which can be used in the preparation of C the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, CR B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a C BARD1, B123, BE2, BE14, BE31 or BE445 mucleic acid sequence, specifically C a wild type BARD1 composition for the detection or purification of BRCA1, C useful to identify a patient having, or at risk of developing cancer. C BARD1 can be used in the preparation of an anti-BARD1 antibody, and in C the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to antibody can be used to identify a patient having or at risk of
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Matches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 287-288; 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-230317/20.
N-PSDB; AAV24135.
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03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BARD1; ring protein; BRCA1; breast cancer; risk; diagnosis
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97US-0042611P.
97US-0042985P.
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Pred. No.
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Query Match

48 . 88 ;

Score 20;

B

2

Length 515

Query Match Best Local Sim Matches 20;

Similarity

48.8%; Score 20; 100.0%; Pred. No. Live 0; Mismatcl

DB 4; Le 4.2e-12;

Length 2144; Indels

Mismatches

0

Gaps

0

Conservative

Sequence 2144

A

Sequence 515

A

developing cancer

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                        The invention is directed to BAP28 polypeptides, BAP28 polynuclectide sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polynuclectides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first CDNA sequence of the BAP28 gene consisting of the exons 1 to 45
                                                                                                                                                                                                                              New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
                                                                                                                                                                                                     Claim 14; Page 297-304; 349pp; English.
                                                                                                                                                                                                                                                                                        N-PSDB; AAF83909,
                                                                                                                                                                                                                                                                                                                               Barry C,
                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1999; 99US-0141323P
18-JAN-2000; 2000US-0176880P
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                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by BAP28 cDNA consisting of exons 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB85029 standard; protein; 2144
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The MAF83909, AAF83910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Gly or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Asp or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Ser or Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Ala or Val
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                                                                                                                                                                                                                                                                                                                            Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٥,
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PR 08-SEP-2000 PR 14-SEP-2000 PR 21-SEP-2000 PR 21-SEP-2000 PR 22-SEP-2000 PR 22-SEP-2000 PR 29-SEP-2000 PR 13-OCT-2000 PR 20-OCT-2000 PR 20-	22-AUG-2000; 2000US-0227109 23-AUG-2000; 2000US-0228974 30-AUG-2000; 2000US-0228974 01-SEP-2000; 2000US-0229347 01-SEP-2000; 2000US-0229347 01-SEP-2000; 2000US-0229347 01-SEP-2000; 2000US-0229347 05-SEP-2000; 2000US-0229351 05-SEP-2000; 2000US-0239047 06-SEP-2000; 2000US-0230437 06-SEP-2000; 2000US-0231244 08-SEP-2000; 2000US-0231244 08-SEP-2000; 2000US-0231244	PR 14-JUL-2000; 2000US-0217496P. PR 26-JUL-2000; 2000US-022963P. PR 26-JUL-2000; 2000US-0220964P. PR 26-JUL-2000; 2000US-0220964P. PR 14-AUG-2000; 2000US-0224518P. PR 14-AUG-2000; 2000US-022513P. PR 14-AUG-2000; 2000US-0225213P. PR 14-AUG-2000; 2000US-0225214P. PR 14-AUG-2000; 2000US-0225266P. PR 14-AUG-2000; 2000US-0225266P. PR 14-AUG-2000; 2000US-0225268P. PR 14-AUG-2000; 2000US-0225279P. PR 14-AUG-2000; 2000US-0225279P. PR 14-AUG-2000; 2000US-022575P. PR 14-AUG-2000; 2000US-022575P. PR 14-AUG-2000; 2000US-0225759P. PR 14-AUG-2000; 2000US-022568P. PR 14-AUG-2000; 2000US-0225679P. PR 14-AUG-2000; 2000US-0225759P. PR 14-AUG-2000; 2000US-025759P. PR 14-AUG-2000; 2000US-025759P. PR 14-AUG-2000; 2000US-025759P. PR 14-AUG-2000; 2000US-025759P. PR 14-AUG	31-JAN-2000; 2000US-0179065 04-FEB-2000; 2000US-0186628 24-FEB-2000; 2000US-0184664 02-MAR-2000; 2000US-018974 17-MAR-2000; 2000US-0199076 18-AFR-2000; 2000US-0199076 18-AFR-2000; 2000US-0199076 18-AFR-2000; 2000US-0209467 07-JUN-2000; 2000US-0209467 28-JUN-2000; 2000US-0218185 30-JUN-2000; 2000US-0216186 30-JUN-2000; 2000US-0216647 07-JUL-2000; 2000US-0216667 07-JUL-2000; 2000US-0216687	XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; KW cytostatic; gene therapy; vaccine; metastasis. XX OS Homo sapiens. XX PN W0200157182-A2. XX PD 09-AUG-2001. XX PF 17-JAN-2001; 2001WO-US001354.	RESULT 4 AAM87229 standard; protein; 118 AA.  XX AC AAM87229,  XX DT 07-NOV-2001 (first entry)  XX DE Human immune/haematopoietic antigen SEQ ID NO:14822.
20000US.	17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;	01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;	02-OCT-2000) 02-OCT-2000) 02-OCT-2000) 02-OCT-2000) 13-OCT-2000) 13-OCT-2000) 20-OCT-2000) 20-OCT-2000) 20-OCT-2000) 20-OCT-2000) 20-OCT-2000) 20-OCT-2000)	25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;	08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

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RESULT 5
ABU24428
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                                                                                                                                                                                                                                                                                                                                                                                             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

C andino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

C activity, and can be used in gene therapy and vaccine production. (I)

C proteins and polynucleotides may be used in the prevention, diagnosis and

C treatment of diseases associated with inappropriate (I) expression. For

C example, they may be used to treat disorders associated with decreased

C expression by rectifying mutations or deletions in a patient's genome

C that affect the activity of (I) by expressing inactive proteins or to

C supplement the patients own production of (I). Additionally, (I)

C polynucleotides may be used to produce the secreted (I), by inserting the

C nucleic acids into a host cell and culturing the cell to express the

C protein. (I) proteins and polynucleotides may be used to prevent,

C diagnose and treat immune/haematopoietic-related diseases, especially

C cancers and cancer metastases of haematopoietic antigen genomic

C sequences from the present invention. AAK54942 to AAK3950 and AAM82169

C represent approach in the areanilification of the present invention
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
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01-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

06-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000

08-DEC-2000
                                                                                  Protein encoded by Prokaryotic essential gene #9955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                            Clostridium botulinum
                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                         19-JUN-2003
                                                                                                                                                        ABU24428
                                                                                                                                                                                   ABU24428 standard; protein; 308
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastass
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                                                                                                                                                                                                                                                                                                                                                                                                                         represent sequences
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                                                                                                                                                                                                                                                                                                                                               Local
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2000US-0251479P.
2000US-0251868P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251980P.
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                     (first entry)
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2000US-0251988P.
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2000US-0250160P.
2000US-0250391P.
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2000US-0249299P
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                                                                                                                                                                                                                                                                                                                                                                                                                       used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                           17.1%; Score 7;
100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                              Mismatches
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o. 24;
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WO200277183-A2

RESULT 6 ABG17089

먉 S

Query Match Best Local S Matches 7

Similarity 100 7; Conservative

17.1%; or 100.0%; Prr

Score 7; ; Pred. No.

DB ( 6

0

0;

Gaps

0

Length 308

Sequence 308 AA;

AXID

ABG17089 standard; protein; 732 AA.

ABG17089;

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of the nucleic acid inhibits proliferation of a cell. Also included are:

(C (1) a vector comprising a promoter operably linked to the nucleic acid conditing a polypeptide whose expression is inhibited by the antisense concluded are:

(C encoding a polypeptide whose expression is inhibited by the antisense concluded are:

(C nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide or its fragment whose expression is inhibited by the containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) clentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the extent compound that inhibits the containing the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for identifying to retain and containing the activity and containing the activity and containing the caseful for identifying to the activity of a compound that inhibits the collection of an organism. The antisense nucleic acids are sensitived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                     identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 52352; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6213 antisense sequences given in the specification where
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Trawick
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2002US-00072851.
2002US-0362699P.
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Carr GJ,
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Forsyth
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Xu HH;
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RESULT 7
ADN73151
ID ADN7
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AC ADN7
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DT 15-J
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                                                                                                                                                                                                                                                                                                                                           creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of diagnostics, forensics, gene mapping, identification of mutations and no produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 47448; 103pp; English
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                                  ADN73151;
                                                                   ADN73151 standard; protein;
                                                                                                                                                                                                                                                                                                Sequence 732 AA;
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(first entry)
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100.0%; Pr
                                                                                                                                                                                                                           17.1%; Score 7; DB . 100.0%; Pred. No. 1e. :ive 0; Mismatches
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                                                                    976 AA
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plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis;
                                                                                                                                                 Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1046.
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Arabidopsis thaliana. nitrogen metabolism; carbon metabolism

WO2004035798-A2

18-OCT-2002; 2002EP-00079408 20-OCT-2003; 2003WO-EP011658

Inze D, De Veylder L, Vlieghe

N-PSDB; ADN73150. WPI; 2004-348466/32.

Altering plant characteristics, useful for producing plants for enzyme opharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins. or

Claim 1; SEQ ID NO 1046; 134pp; English

CC This invention relates to a novel method for altering one or more plant CC characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric CC E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes CC generating transgenic plants for the production of growth regulators, cC enzymes, therapeutics, pharmaceuticals and animal feed products, where CC the altered plant characteristics are selected from increased yield or CC biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, blochemistry, signal CC transduction, storage lipid mobilisation and/or altered photosynthesis, ceach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers CC during transformation of cells or tissues. The identified genes play a complete transcription factors. This polypeptide sequence is thale cress protein capressed by a gene upregulated 1.3 fold or more in plants overexpressing CC invention.

Sequence 976 AA;

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RESULT 8
ADNO4625
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                                                               ADN04625 standard; protein; 2000 AA.
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                                                                                                                             32 KEEKNVL 38
                                                                                                             KEEKNVL 480
                                                                                                                                                Conservative
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                                                                                                                                                        Score 7; DB 8; Le
Pred. No. 1.3e+02;
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Antipsoriatic protein sequence #498

01-JUL-2004 (first entry)

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THE PRESENTATION OF THE PR
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AAM39043
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Best Local S
Matches 7
23-DEC-1999;
21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic add is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                         26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                           WO200153312-A1
                                                                                                                                                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-305105/28
N-PSDB; ADN04624.
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                       99US-00471275.
2000US-00488725.
2000US-00552317.
2000US-00598042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
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RESULT 10
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Best Local S
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                                                                                                                                                               UDP-N-acetylglucosaminie i control transferase;
CTP:CMP-3-deoxy-D-manno-octulosonate transferase;
UDP-N-acetylmuramylalanyl-D-glutamate-2-6-diaminopimelate ligase;
UDP-N-acetylpuyruvoylglucosamine reductase;
UDP-N-acetylglucosamine pyrophosphorylase;
UDP-N-acetylglucosamine pyrophosphorylase;
UDP-N-acetylmuramoylalanine-D-glutamate ligase;
UDP-N-acetylmuramoylalanine ligase; aspartate semialdehyde dehydrup-N-acetylmuramoylalanine ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune systems suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                         epitope; antibacterial;
UDP-N-acetylglucosamine 1-carboxyvinyl transferase-1;
CTP:CMP-3-deoxy-D-manno-octulosonate transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-alanine:D-alanine adding
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Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL46346 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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N-PSDB; AAI58199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 central nervous system injuries.
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Wang Z,
Goodrich
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2000US-00727344
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Wehrman T,
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100.0%
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Xu C,
IC RT;
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Pred. No.
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Yang Y,
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Zhang ,
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, Zhao QA;
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WO2003087353-A2

Pseudomonas

aeruginosa

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RESULT 11
AAM89273
ID AAM89
XX
AC AAM89
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                                                                                                                                                                                     CC The invention relates to isolated, recombinant polypeptides (I) that have CC at least one activity of specified bacterial enzymes involved in cell CC membrane biogenesis. (I) are: UDP-N-acetylglucosamine 1-carboxyvinyl CC transferase-1 of Streptococcus pneumoniae (S.p.), Pseudomonas acruginosa (P.a.) or Staphylococcus aureus (S.a.) CTP.CMP-3-deoxy-D-manno-CC octulosonate transferase of Escherichia coli (E.c.) or Haemophilus CC influenzae (H.i.); UDP-N-acetylmuramylalanyl-D-glutamate- 2.6-CC diaminopimelate ligase of P.a.; D-alanine:D-alanine adding enzyme of S.a. CC or P.a.; D-alanine-D-alanine ligase of Enterococus faecalis (E.f.); UDP-N-CC acetylguyruvylglucosamine reductase of P.a. or H.i.; UDP-N-CC acetylguyruvylglucosamine ligase of E.f., H.i. or S.a.; UDP-N-CC acetylmuramoylalanine-D-glutamate ligase of E.f. or H.i.; UP-N-CC acetylmuramotylalanine-D-glutamate ligase of E.f. or H.i.; DP-N-CC acetylmuramate:alanine ligase of E.c.; and aspartate semialdehyde CC dehydrogenase of H.i and UDP-N-acetylmuramotylalanyl-D-glutamate (sic) of CC analysis) the structural coordinates (by X.ray diffraction CC analysis) the structural coordinates (by X.ray diffraction CC analysis) the structural coordinates (by X.ray diffraction CC design modulators of (I), potential therapeutic agents for treating CC diseases caused by the specified bacteria. This sequence represents an CC epitope from one of the proteins of the invention.
                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conser
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09-APR-2002

09-APR-2002

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31-MAY-2002

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27-DEC-2002
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Beattie |
Virag C,
 AAM89273;
                    AAM89273 standard; protein; 32
                                                                                                                                                                    Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 64; 407pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant bacterial enzymes involved in cell membrane biogenesis, useful for designing potential antibacterial agents.
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B, Mansoury K, Ouyang H,
, Buzadzija K, Pinder B,
ajah D, Thalakada R;
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                                                                              PEVPVL 19
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2002US-0436568P.
2002US-0436734P.
2002US-043685P.
2002US-0436885P.
2002US-0436889P.
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2002US-0385283P.
2002US-0386283P.
2002US-04240348P.
2002US-0425200P.
2002US-0425200P.
                                                                                                                        Conservative
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                                                                                                                       14.6%; Score 6; DB
100.0%; Pred. No. 69
Live 0; Mismatches
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Vallee F, Richards D, Nethery K;
Alam MZ, Tai M, Canadien V;
                                                                                                                                    DB 7;
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07-UN-2000
28-JUN-2000
30-JUN-2000
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07-JUL-2000
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14-JUL-2000
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16-SEP-2000
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2000US-0230438P.
2000US-0231242P.
2000US-0231243P.
2000US-0231244P.
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2000US-0227009P.
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2000US-0229287P.
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2000US-0225213P
2000US-0225214P
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2000US-0225266P
2000US-0225267P
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2000US-0225267P
2000US-0225447P
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2000US-0225758P
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2000US-0215135P.
2000US-0216647P.
2000US-0216647P.
2000US-0217487P.
2000US-0217487P.
2000US-0217496P.
 2000US-0231968P.
2000US-0232397P.
2000US-0232398P.
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2000US-0232081P
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2000US-0229513P.
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2000US-0220963P.
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2000US-0205515P.
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14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000;

2000US-0233063P 2000US-0233064P

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21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000

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RESULT 12
AAM20415
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 Query Match
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Matches 6
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
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N-PSDB; AAK62054.
 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                        Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer.
                                                                                                                                                                                                                                  Peptide #6849 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                               AAM20415;
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                                                                        30-JAN-2001;
                                                                                                   09-AUG-2001.
                                                                                                                                 WO200157278-A2
                                                                                                                                                            Homo sapiens.
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6; Conserva
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); 2001US-0259678P.
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
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08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US 0246532P 2000US 0246610P 2000US 0246611P 2000US 0246611P 2000US 024920P 2000US 024920P 2000US 024920P 2000US 0249211P 2000US 0249214P 2000US 0249214P 2000US 0249214P 2000US 0249214P 2000US 0249214P

17.NOV-2000; 17.NOV-2000; 17.NOV-2000; 01.DEC-2000; 01.DEC-2000; 05.DEC-2000; 05.DEC-2000; 05.DEC-2000; 06.DEC-2000; 08.DEC-2000;

2000US-0249264P. 2000US-0249265P. 2000US-0249297P.

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RESULT 13
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ID ABB41
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26-MAY-2000;
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Heia cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical spithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe
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b; Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver single exon probe.
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Human genome-derived single exon nucleic acid gene expression in human fetal liver.

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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by on such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta
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04-OCT-2000;
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; 2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, by measuring gene expression, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
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                                                      30 ERKEEK 35
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      ERKEEK 38
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                                                                                                                  Conservative
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                                                                                                               14.6%; Score 6; DB 4; Lei
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.3e+02; mismatches 0;
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                                                                                                                                                                           Length 47;
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Search completed: February 1, 2005, 15:20:10 Job time : 71.7778 secs

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_RUW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_RUW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_RUW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_RUW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_RUW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US10_PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US10_PUB.pep:*
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Gapop 60.0 , Gapext 60.0
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41
1 LKLLCKNFGAENPDPFVPVL.....TAVKLIAPERKEEKNVLGSA 41
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2 3 4 4 6 6 7 7 10 11 11 11 12	Result No.
71777777777	Score
17. 17. 17. 17. 17. 17. 17. 17. 17.	Query Match
61 75 79 93 98 119 169 186 232 232 232 308	Query Match Length DB
15 15 15 15 15 15 15 15	DB :
US-10-767-701-52614 US-10-424-599-1274449 US-10-424-599-157348 US-10-424-599-198515 US-10-424-599-271135 US-10-424-599-279781 US-10-424-599-279781 US-10-424-599-157336 US-10-424-599-157336 US-10-424-599-157334 US-10-282-122A-52352 US-10-369-493-924	ID US-10-128-558-167
5261 2244 1573 1985 2711 2731 5390 5390 5797 1573	Description Sequence 167, App

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101	98	98	95	95	92	92	90	85	79	79	74	72	71	70	70	69	68	67	67	64	62	61	55	53	50	50	50	47	4.	574	
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-10-437-963-17084	-10-425-115-319	-10-425-115-24904	-10-296-115-145	0-424-599-193	14	-10-424-599-17159	-10-437-963-146	-10-425-115-26929	0-425-115-30835	-10-425-115-293	-10-424-599-1875	44	-424-599-2384	US-10-427-348-49	880-192-4	-10-425-115-264	-10-767-701-6121	-10-424-599-218	-10-156-761-82	-10-425-115-335	-10-282-122A-4805	344	-10-424-599-25	0-425-115-285	-25	US-10-242-515-1063	-764-877-106	09-864-761-	-10-437-963-15206	3-109	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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## ALIGNMENTS

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Remai	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	CURRE	CURRE	FILE	TITLE	TITLE	APPLI	APPLI	APPLI	APPLI	APPLI	GENERA	Public	Sequen	RESULT 1 US-10-12
Remaining Prior Application data removed - See File Wrapper or PALM		FILING DATE: 2001-02-05	PRIOR APPLICATION NUMBER: PCT/US01/03800	PRIOR FILING DATE: 2000-04-27	PRIOR APPLICATION NUMBER: US 09/560,875	PRIOR FILING DATE: 2000-02-03	PRIOR APPLICATION NUMBER: US 09/496,914	PRIOR FILING DATE: 2001-01-25	PRIOR APPLICATION NUMBER: PCT/US01/02623	PRIOR FILING DATE: 2000-01-25	PRIOR APPLICATION NUMBER: US 09/491,404	PRIOR FILING DATE: 2000-12-22	PRIOR APPLICATION NUMBER: PCT/US00/35017	PRIOR FILING DATE: 2000-04-25	PRIOR APPLICATION NUMBER: US 09/552,317	PRIOR FILING DATE: 2000-01-21	PRIOR APPLICATION NUMBER: US 09/488,725	PRIOR FILING DATE: 2001-12-11	PRIOR APPLICATION NUMBER: US 60/339,453	CURRENT FILING DATE: 2002-04-22	CURRENT APPLICATION NUMBER: US/10/128,558	FILE REFERENCE: 812A	TITLE OF INVENTION: Polypeptides	TITLE OF INVENTION: Novel Nucleic Acids and	APPLICANT: Drmanac, Radoje T	APPLICANT: Boyle, Bryan J	APPLICANT: Weng, Gezhi	APPLICANT: Wang, Zhiwei	APPLICANT: Tang, Y. Tom	ž		Sequence 167, Application US/10128558	RESULT 1 US-10-128-558-167
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5323)B CURRENT FILIC DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 224449
LENGTH: 75
TYPE: prom
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US-10-128-558-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Clone ID: 12691726.pep
US-10-767-701-52614
                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-224449
                                                     US-10-424-599-224449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: pt FL genes Version 6.0
SEQ ID NO 167
LENGTH: 1149
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Publication No. US20040172684A1
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Best Local
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LENGTH: 61
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
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CURRENT FILING DATE: 2004-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                  ORGANISM: Glycine max FEATURE:
                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_44706C.1.pep
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 17.1%;
100.0%;
Score 7; I
Pred. No.
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   DB 15;
lo. 21;
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                  Length 75;
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US-10-424-599-157348
; Sequence 157348, Application US/10424599
; Publication No. US20040031072A1
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Best Local Similarity
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_113105C.1.pep
US-10-424-599-157348
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                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_21283C.1.pep
US-10-424-599-198515
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Solvucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FILE REFERENCE: 38-21(5323)B
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                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 198515
LENGTH: 93
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                                     Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 198515, Application US/10424599 Publication No. US20040031072A1
                                                                       Query Match
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APPLICANT: LA ROSA Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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NAME/KEY: unsure
LOCATION: (1)...(79)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                 FEATURE:
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   29 PERKEEK 35
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7; Conserva
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                                       Conservative
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                                                        100.0%;
                                       b; Score 7; DB 1
b; Pred. No. 25;
0; Mismatches
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Pred. No.
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70. 22;
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RESULT 8
US-10-767-701-53909
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US-10-424-599-283405
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
FULE REFERENCE: 38-21(5322)B
FULE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 271135
LENGTH: 98
TYOPE: DET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 283405
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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CURRENT FILING DATE: 2003-04-28
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TYPE: PRT
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NAME/KEY: unsure
LOCATION: (1)..(119)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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nes 7; Conservative
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RESULT 10
US-10-424-599-157336
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
FULE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 53909
LENGTH: 169
LENGTH: 169
                                                                                                                                       Query Match
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 279781
LENGTH: 186
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(186)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT_MRT3847_94664C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Glycine
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ORGANISM: Sorghum bicolor
FEATURE:
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100.0%; Pred. No. 46
ive 0; Mismatches
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Pred. No. 42;
0; Mismatches
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Sequence 157336, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K

Kovalic David | Zhou Yihua Cao Yongwei

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US-10-282-122A-52352
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Best Local Similarity
7; Conserv
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285884
SEQ ID NO 157336
LENGTH: 232
TYPE: PRT
ORGANISM: Glycine max
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 157334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao Yongwei
TITLE OF INVENTION: SQU Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
GURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
UMMBER OF SEQ ID NOS: 285684
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APPLICANT: Kovalic David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 38-21 (53223) B
                                                                                                         APPLICANT:
                                                                                                                                          APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                        APPLICANT:
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                                                                      APPLICANT
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Zhou Yihua
                                                                                                                                                         Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                        Ohlsen, Kari
Zyskind, Judith
                                                                                     Trawick, John
                               Forsyth, R.
                                                   Yamamoto, Robert
                                                                Carr, Grant
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                                                                                                         Daniel
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100.0%; Pred. No.
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Pred. No.
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o. 56;
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 924
LENGTH: 380
TYPE: PRT
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                                                                                                                        ; ORGANISM: Archaeoglobus fulgidus US-10-369-493-924
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US-10-369-493-924
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SEQ ID NO 52352
LENGTH: 308
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Best Local
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APPLICANT: Hink:
APPLICANT: Slat.
                                         Matches
                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/242,578
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18 PVLNTAV 24
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100.0%; Pred. No.
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APPLICANT: Boukharov, Andrey ...
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERIOR: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 2004966
SEQ ID NO 109624
LENGTH: 574
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
FORMATION: Clone ID: PAT_MRT4530_13764C.l.pep
US-10-437-963-109624

17 1%: Score 7; DB 16; Length 574;
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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CURRENT FILING DATE: 2003-05-14
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NAME/KEY: unsure
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OTHER INFORMATION: unsure at all Xaa locations
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TYPE: PRT
ORGANISM: Oryza sativa
                                         / Match 17.1%; Score 7; DB 16; Length 574; Local Similarity 100.0%; Pred. No. 1.2e+02; nes 7; Conservative 0; Mismatches 0; Indels
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Barbazuk, Brad
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Search completed: February 1, 2005, 15:44:47 Job time: 60.7778 secs

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Post-processing: Listing first 45 summaries
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35360
                                                                                                                                                                                                                                                                                                                                                                3-ketoacyl-CoA thiolase (acaB-6) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #text_change 09-Jul-2004 C;Date: 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: B69275
C;Accession: B69275
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, S.; Fleischmann, R.D.; Quackenbush, G.G.; Gill, G.G.; Gi
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                                                                                                                                                                                                              Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9XAL0;
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC66T3.03
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A;Reference number: Z21576
A;Accession: T35360
S
                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Roseidues: 1-380 <KLE>
A;Cross-references: UNIPROT:030037; GB:AE001092; GB:AE000782; NID:g2689415; PIDN:AAB9102
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Scoring table:

Gapop 60.0 , OLIGO

Word size : Searched:

0

Title: Perfect score:

SEQSASN1694

Sequence:

Run on:

Copyright

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A;Cross-references UNIPROT: P39217; GB:L29189; NID: 9459687; PIDN: AAA20557.1; PID: 9459691
A;Note: authors translated the codon CAG for residue 10 as Trp
A;Note: authors translated the codon CAG for residue 10 as Trp
C; Bron, S; Broullet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sakot, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Zamstein, E.; Yoshikawa, H.; Danchin, A.
A;Reference number: A69580; MUID: 98044033; PMID: 9384377
A;Accession: A69724
A. Cetession: A69724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate name8: chemotax18 transducer nomotoy .urc C;Specie8: Bacillus subtilis C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C;Accession: D54078; A69724 R;Hanlon, D.W.; Ordal, G.W. R;Hanlon, D.W.; Ordal, G.W. 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein - Thermotoga maritima (strain MSB8 C;Species: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               문
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A;Cross-references: UNIPROT:Q9WXV3; GB:AE001696; GB:AE000512; NID:g4980582; PIDN:AAD351
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garrett, M.M.; Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: B72418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methyl-accepting chemotaxis protein tlpB - Bacil
N;Alternate names: chemotaxis transducer homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A72200;
A;Accession: B72418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title: Cloning and characterization of g
Reference number: A54078; MUID:94245722;
Accession: D54078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Superfamily: GTP-binding protein obg; translation elongation; 165-290/Domain: translation elongation factor Tu homology <ET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: TM0098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-662 <HAN>
Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342
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acid sequence not shown; translation not shown
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A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 7;
100.0%; Pred. No.
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MUID:99287316; PMID:10360571
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>molog TLPB
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A;Gene: tlpB
C;Superfamily: probable methyl-accepting
C;Keywords: transmembrane protein
                                                                     A;Cross-references: GB:Z99119; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15112.
A;Experimental source: strain 168
C;Genetics:
                            chemotaxis
                              transducer
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Matches
                                         Query Match
                                     Local
278 PVLNTAV 284
               18 PVLNTAV 24
                           l Similarity
7; Conserv
                             Conservative
                                     100.0%;
                                             17.18;
                                            Score 7;
                                    Pred. No.
                                 DB 20;
                                            2
                              0
                                            Length 662
                              0;
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J. Mol. Biol. 214, 39-53, 1990
A;Title: Nucleotide sequence of the promoter-distal region of A;Reference number: S10658; MUID:90317835; PMID:2164585
                                                                                                                                                  C;Date: 30-Jun-1990 #sequence revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: S10660; PS0322; PS0321; PS0068; T00299; T42198 R;Yoshioka, Y.; Fujita, Y.; Ohtsubo, E.
                                                                                                                                                                                                                                                                               C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                          DNA helicase I (EC 3.6.1.-) - Escherichia coli plasmids
A;Accession: S10660
                                                                                      the tra operon of plasmid
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A,Title: Sequence and conservation of genes at the distal end A,Reference number: JQ1338; MUID:92009201; PMID:1916281 A,Accession: PS0322 A;Residues: 1-1756 <YOS>
A;Cross-references: UNIPROT:P22706;
A;Experimental source: plasmid R100 R;Cram, D.S.; Loh, 1991 S.M.; Cheah, K.C.; Skurray, EMBL: X55815; NID: g42620; PIDN: CAA39337.1; PID: g42623 of the transfer region on

A; Molecule type: DNA A; Residues: 1747-1756 < CRA2> A;Accession: A; Experimental source: plasmid A;Cross-references: GB:M38048 A; Molecule type: DNA A; Residues: 1747-1756 < CRA1> PS032 R6-5 NID:g148651; PIDN:AAA98090.1; PID:g148652 F

A;Cross-references: GB:M38047; A;Experimental source: plasmid R;Jalajakumari, M.B.; Manning, Gene 81, 195-202, 1989
A;Title: Nucleotide sequence of the traD region in the Escherichia coli F sex factor.
A;Reference number: JS0293; MUID:90034191; PMID:2680768 P.A.

A;Molecule type: DNA
A;Residues: 1,'M',3,'IAQ',7,'R',9-35,'R',37-68,'CRMAVTR',76-150 <JAL>
A;Residues: 1,'M',3,'IAQ',7,'R',9-35,'R',37-68,'CRMAVTR',76-150 <JAL>
A;Cross-references: GB:M29254; NID:g148618; PIDN:AAA83930.1; PID:g551859
A;Experimental source: strain K12; F factor
A;Note: the authors translated the codon CTG for residue 41 as Glu
R;Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsud A; Accession: PS0068

DNA Res. 5, 1-9, 1998 A;Title: Complete nucleotide sequences of 93-kb and 3.3-kb A;Reference number: Z14127; MUID:98290540; PMID:9628576 A;Accession: T00299 plasmids K.; Yatsudo, of. an enterohemorrhag H.C.; Kubota,

A;Molecule type: DNA, 1109, 'F', 1111, 'G', 1113, 'FN', 1295-1301, 'R', 1303-1309, 'Q', 1311-1332, 'E', A;Residues: 'S', 1108-109, 'E', 1698-1699, 'VTS', 1703-1715, 'P', 1717-1719, 'R', 1721-1726, 'V', 'N', 1632-1682, 'R', 1684-1696, 'E', 1698-1699, 'VTS', 1703-1715, 'P', 1717-1719, 'R', 1721-1726, 'V', A;Cross-references: EMBL:AB011549; PIDN:BAA31818.1.
A;Cross-references: EMBL: A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Reference number: Z22068; MUID:98391744; PMID:9722640 preliminary; translated from GB/EMBL/DDBJ

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A;Cross-references: GDB:56487; OMIM:600261

A;Map position: 6p21.3-6p21.3

C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homolymords: extracellular matrix; glycoprotein

E;Keywords: extracellular matrix; glycoprotein

E;435-461/Domain: EGF homology <EGF>
F;748-828/Domain: fibronectin type III repeat homology #status aty;
F;829-856/Domain: fibronectin type III repeat homology <3F3>
F;973-953/Domain: fibronectin type III repeat homology <3F4>
F;975-1055/Domain: fibronectin type III repeat homology <3F5>
F;1167-1247/Domain: fibronectin type III repeat homology <3F6>
F;1167-1247/Domain: fibronectin type III repeat homology <3F6>
F;1248-1317/Domain: fibronectin type III repeat homology <3F6>
F;1412-1492/Domain: fibronectin type III repeat homology <3F8>
F;1412-1492/Domain: fibronectin type III repeat homology <3F9>
F;1510-1590/Domain: fibronectin type III repeat homology <3F9>
F;1510-1590/Domain: fibronectin type III repeat homology <3F9>
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A;Residues: 'M',1326-1332,'P',1334-1335,'T',1337-1352,'G',1354-1375,'G',1377-1385,'A',1:
A;Residues: 'M',1721-1726,'V',1728-1738,'M',1740-1756 <BUR>
A;Crose-references: EMBL;AF074613; PIDN:AAC70166.1
A;Experimental source: strain EDL933; serotype O157:H7
C;Comment: This is one of the proteins that control the transfer of F plasmid.
C;Comment: There seems to be some variation or dissagreement regarding the translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA, A; Molecule type: mRNA, A; Residues: 2748-3199, 'V', 3201-3299, 'E', 3299-3314, 'G', 3316-3566 < MOR> A; Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 < MOR> A; Rosel (Comparison of Comparison o
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A;Cross-references: UNIPROT:P22105; UNIPROT:QSUC11; EMBL:X71937<br/>
A;Cross-references: UNIPROT:P22105; UNIPROT:QSUC11; EMBL:X71937<br/>
A;Cross-references: UNIPROT:P22105; UNIPROT:QSUC11; EMBL:X71937<br/>
A;Marcell Residues: Sci. U.S. A. (5582-5586, 1989)<br/>
A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/A;Reference number: A33725; MUID:89367293; PMID:2475872<br/>
A;Accession: A33725; MUID:89367293; PMID:2475872
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A;Residues: 1849-1936 <MAT>
A;Experimental source: clone
A;Experimental source: clone
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A;Accession: C42175
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A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the human A;Reference number: A40701; MUID:93300909; PMID:7686164
A;Accession: A40701
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;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004;Accession: A40701; A33725; C42175
;Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.
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conserved hypothetical protein aq_064c - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Accession: C70306 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grain, C.; Canada, C.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grain, C.; Canada, C.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grain, C.; Canada, C
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C70306
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A;Title: Genome sequences of Chlamydia trachomatis MoPn
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F;1678-1749/Domain:
F;1751-1831/Domain:
A;Status: preliminary; nucleic acid sequence not A;Molecule type: DNA A;Residues: 1-77 <AQF>
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homology <3F22>
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homology <3F18>
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A;Cross-references: UNIPROT:P49446
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens,
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: B61180; S40283
R;Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A;Title: Identification of novel protein tyrosine phosphatases of hematopoi
A;Reference number: A61180; MUID:92032882; PMID:1932742
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A;Molecule type; DNA
A;Residues: 1-105 <KLB>
A;Residues: 1-105 <KLB>
A;Cross-references: UNIPROT:O51595; GB:AE001166; GB:AE000783; NID:g2688571; PIDN:AAC6699
A;Experimental source: strain B31
C;Superfamily: yajC protein
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                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-109 <YIA>
                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A61180;
A;Accession: B61180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon - mouse (fragment) N; Alternate names: protein-tyrosine-phosphatase PTPTY8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease
A;Reference number: A70100; MUID:98065943; P
A;Accession: B70181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein BB0651 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
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C;Superfamily:
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A;Experimental source: strain VF5
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                                                                                                                                                       Reference number: S40280
                                                                                                                                   Molecule type: mRNA
                                                                                                                                                                                                Description: Assessment of the
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100.0%; Pred. No.
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hypothetical protein Atu3582 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Ju1-2004 C;Accession: AD2997 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Cher erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li
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C; Keywords: y-; --.
F;12,42,120/Active site: H18, Lys, --.
F;27-85,41-96,59-111,66-73/Disulfide bonds:
                                                                                                     A;Cross-references: UNIPROT:P16414
A;Note: the source is designated as Sp:
C;Superfamily: pancreatic ribonuclease
C;Keywords: 9lycoprotein; hydrolase
E;12,42,120/Active site: His, Lys, His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Murphy, L.; Harris, D.; Parkhill, submitted to the EMBL Data Library, A;Reference number: Z21548
                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-125 < SCH>
                                                                                                                                                                                                                           A; Title: The amino-acid sequence of pancreatic ribonuclease A; Reference number: S04503; MUID:89374807; PMID:2673297
                                                                                                                                                                                                                                                                                                 pancreatic ribonuclease (EC 3.1.27.5) - Ehrenberg's mole-rat
C;Species: Spalax leucodon ehrenbergi (Ehrenberg's mole-rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
                                                                                                                                                                                                                                                                      C;Accession: S04503; A32505
R;Schueller, C.; Neuteboom, B.; Wuebbels,
                                                                                                                                                                                                                                                                                                                                                      S04503
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A; Residues: 1-114 < MUR>
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A;Experimental source: strain A3(2)
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14 DPFVPV 19
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January 1998
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                                            DB 2;
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48;
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; Chen, L.; Kutyavin, T

Wood, G.E.; Chen, C.; Levy, R.; Li,

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; Woo, L McClella

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RESULT 15
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A;Residues: 1-139 <KUR>
A;Residues: 1-139 <KUR>
A;Cross-references: UNIPROT:Q8U9Z3; GB:AE008689; PIDN:AAL44394.1; PID:g17741992; GSPDB:
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: Atu3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AD2997
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A; Map position: linear chromosome
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A; Residues: 1-141 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E98286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AGR_L_2491 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct.-2001 #sequence_revision 22-Oct.-2001 #text_change 09-Jul-2004 C;Accession: E98286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                 A;Map position: 5
A;Introns: 22/3; 76/3; 111/2
                                                                               A;Molecule type: DNA
A;Residues: 1-142 <SAT>
A;Cross-references: UNIPROT:Q9LF19; EMBL:AL391148
A;Experimental source: cultivar Columbia; BAC clone T21H19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8U9Z3; GB:AE007870; PIDN:AAK89815.1; PID:g15159745; GSPDB:
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Local Similarity 100.0%; Pred. No. 58,
nes 6; Conservative 0; Mismatches
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llarity 100.0%; Pred. No. 57
Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 16 FVPVLN 21
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Db 100 FVPVLN 105
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Search completed: February 1, 2005, 15:33:00 Job time: 13.5556 secs

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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q75g97 oryza sativ
Aas98496 oryza sat
Q821y1 chlamydophi
Q9lmw4 arabidopsis
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Q8n717 homo sapien
Q8n717 homo sapien
Q9gm44 macaca fasc
Q6p197 homo sapien
Aah65205 homo sapien
Aah65205 homo sapien
Aah65205 homo sapien
Aah65205 homo sapien
Q87zn5 pseudomonas
Q8bhy7 mus musculu
Q8cfv3 mus musculu
Q8cg69 staphylococ
Q6dji5 xenopus lae
Q89a2 clostridium
Q9xa10 streptomyce
Q8tsu2 methanosarc
Q6ing9 xenopus lae
Aah72312 xenopus la
Q30037 archaeoglob
Q9wxv3 thermotoga
Q95kc0 macaca fasc
Q8kbw0 chlorobium
Q610f3 picrophilus
Q6dik6 xenopus tro
Q6zn26 homo sapien
Bad18549 homo sapien
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DT 16-OCT-200 DT 05-UTL-200 DE Protein BJ GN Name-BAP20 OS Homo sapio OC Eukaryota OC Eukaryota OC Mammalia; OX NCBI_TaxII RN [1] RP SEQUENCE I RP SEQUENCE	28 28	0 C C C C C C C C C C C C C C C C C C C
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EMBL; AX116105; CAC15948.1; -.
EMBL; AX012121; BAA91564.1; ALT INIT.
EMBL; AX081221; BA931564.1; ALT
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ40893.
Hymon sapiens (Human)
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Ota T., Suzuki Y.,
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Mammalia; Eutheria;
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Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Xa Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
Xa Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
Xa Onitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Xa Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Xa Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Xa Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Xa Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Xa Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
"Complete sequencing and characterization of 21,243 full-length human
Query Match
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Matches 20
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16-OCT-2001 (Rel. 40, Last seq
01-OCT-2004 (Rel. 45, Last ann
Protein BAP28 (QnpA-17571) (Fr.
Name=BAP28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK098212; BAC05261.1; -. InterPro; IPR008938; ARM. SEQUENCE 897 AA; 101574 MW;
                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9GM44;
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                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                     SEQUENCE
                                                                                                                                                                          PROSITE; PS50077; HEAT_REPEAT; FALSE_NEC
                                                                                                                                                                                                         InterPro; IPR008938; ARM. InterPro; IPR000357; HEAT
                                                                                                                                                                                                                                                                EMBL; AB049842; BAB16728.1; ALT_INIT.
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958 AA;
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100.0%;
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                                                       Length 958;
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RA Klausner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Ra Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Cararinci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Cararinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raha Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rodriguez A.C., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Rodriguez G. T. Marra M. A.
                                                                                                                                                                                                                                                                                                            Matches
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                                       AAH65205 PRELIMINARY;
AAH65205;
02-MAR-2004 (TrEMBLrel. 27, C:
02-MAR-2004 (TrEMBLrel. 27, L:
02-MAR-2004 (TrEMBLrel. 27, L:
FLJ10359 protein (Fragment).
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 Eukaryota, Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2004) to the EMBL; BC065205; AAH65205.1;
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MEDLINE=22388257;
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Mammalia; Eutheria; Primates;
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05-JUL-2004
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                  sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                 1106 AA;
                                                                                                                                                                                                                                                                                                            Conservative
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Feingold E.A., Grouse L.
 Chordata;
                                                                                                                                                                                                                                                                                                                         48.8%;
100.0%;
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases.
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 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                            Mismatches
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A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Interest C., RA Electron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA RAS.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Matches 20
            Deng W.-L., Ramos A.R., Alrano J.R., Schneider Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider Bender C.L., White O., Fraser C.M., Collmer A.; "The complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the Arabidopsis and the complete genome sequence of the complete genome sequence of the complete genome sequence genome sequence of the Arabidopsis and the complete genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence gen
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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.A. 100:10181-10186(2003).
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TIGR; PSPT03389;
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GO; GO:0016998; P:cell wall catabolism; IEA.
GO; GO:0006032; P:chitin catabolism; IEA.
GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
InterPro; IPR000726; Glyco_hydro_19.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=20530913, PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Naga
                                                                                                       carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Y., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Hippocampus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN-C57BL/6J; TISSUE-Hippocampus;
MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAR-2004 (TrEMBLrel.
Mus musculus adult male
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01-MAR-2003
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ProDom; PD354900; Glyco_hydro_19; 1.
                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUE-Hippocampus; MEDLINE-20499374; PubMed-11042159; Carninci P., Shibata Y., Hayatsu N.,
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1003 (TrEMBLrel. 23, Last sequence update)
1004 (TrEMBLrel. 26, Last annotation update)
10104 (TrEMBLrel. 26, Last annotation update)
10104 adult male hippocampus cDNA, RIKEN full-length enriched
10106:C630007C17 product:weakly similar to HYPOTHETICAL 52.2
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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A Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,

A Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

A Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,

James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

A Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M.,

Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J.,

"Complete genomes of two clinical Staphylococcus aureus strains:

Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

EMBL, BX571856, CAG41433.1; -.

DR InterPro, IPR009057; Homeodomain_like.

DR InterPro, IPR009057; Homeodomain_like.
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Best Local (
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Best Local
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Q6GE69;
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035535; AAH35535.1; -
MGD; MGI:2442949; C630007C17Rik.
NON TER
1
1
103331 MW; 1C8DA479216BA70C CRC64:
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  Q6DJ15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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05-JUL-2004
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7; Conserv
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PRELIMINARY;
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Bacillales; Staphylococcus
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0; Mismatches
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Last annotation update)
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pred. No.
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RESULT 11
ISPE CLOTE
ID TISPE CLOTE STANDARD; PRT; 280 AA.
AC Q899A2;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC Q8 (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase (EC Q8 (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase (EC Q8 Name=ispE; OrderedLocusNames=CTC00283;
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clost
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

B Carrinci P., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,

A Blosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Tokenman J.W., Green E.D., Dickeon M.C.,

B Lakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
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01-OCT-2004 (TrEMBLrel. 28,
01-OCT-2004 (TrEMBLrel. 28,
01-OCT-2004 (TrEMBLrel. 28,
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Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 209 AA; 23557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC075194; AAH75194.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S.L., St
Richardson P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917;
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"Generation and initial analysis of more than 15,000 full-length human
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Strausberg R.L., Feingold E.A., Grouse L.H.,
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                                                                                                                                                                                                                                                                                              156 KNFGAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                              162
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                                                                                                                                                                                                                                                                                                                                                                           17.1%; Score 7; DB 100.0%; Pred. No. 51 100.0%; Mismatches
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              B52BF04AB345B3B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   DB .
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pontius J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 209
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                                                                    (EC 2.7.1.148)
kinase).
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NCBI\_TaxID=1513; Clostridium

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RESULT 12
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Best Local S
Matches 7
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HAMAP; MF 0006204; GHMP kinase.

InterPro; IPR0008204; Homoser_kin.

InterPro; IPR0004244; Ispb.

Pfam; PF00288; GHMP kinases; 1.

PRINTS; PR00958; HOMSERKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Massachusetts / E88;

STRAIN=22457353; PubMed=12552129; DOI=10.1073/pnas.0335853100;

MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;

Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H

Brueggemann H., Beaumer S., Pricke W.F., Wezer A., Liesegang H

Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT SITE
ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tetanus disease.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser
                                                                                                                                                  Putative membrane protein. OrderedLocusNames=SCO3592;
                                                                                                                                                                                                                                           Q9XAL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE015936; AAO34927.1; -.
                                           SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
                                                                                                                                  Streptomyces coelicolor
                                                                                                                                                                                                               01-NOV-1999
                                                                                                                                                                                                                             Q9XAL0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase.
                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Complete proteome; Isoprene biosynthesis; Kinase;
                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'IGRFAMB; TIGR00154; ispE;
                                                                                                       treptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-perythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anus disease.";

: Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).

FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy

group of 4 diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the GHMP kinase family. IspE subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome sequence of Clostridium tetani, the causative agent of
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7; Conserv
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280 AA;
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19
                                                                                                       Streptomycetaceae; Streptomyces
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Last annotation updat
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By similarity.
By similarity.
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Query Match
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Matches 7
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01-JUN-2002
01-OCT-2003
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-C2A / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

MEDLINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

MEDLINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

MEDLINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

MEDLINE-21929760; MacConnal P.

Galagan J.E., Nacdounal P.

FitzHugh W., Calvo S., Engels R., Endrizzi M.G., Macconna R.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., NcEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,

Springer T.A., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,

Petry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein MA07
OrderedLocusNames=MA0703;
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PIR; T35360; T35360.
InterPro; IPR005135; Exo_endo_phos.
Pfam; PF03372; Exo_endo_phos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hopwood
                                                                                                                                EMBL; ABO10731; AAM04143.1; -.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0006260; P:DNA replication; IEA.

InterPro; IPR003141; Pesterase PHP N.
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                                                                   Complete proteome; Hypothetical SEQUENCE 334 AA; 38654 MW; 1
                                                                                                     Pfam; PF02231; PHP N; 1.
SMART; SM00481; POLITIAC; 1.
                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                Pritchett M., Sowers K.R., Metcalf W.W., Birren B.;
                                                                                                                                                                                                                               Genome Res.
                                                                                                                                                                                                                                                               "The genome of Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2214;
                                                                                                                                                                                                                             physiological diversity."; ome Res. 12:532-542(2002).
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 Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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   Score 7; DB 2; Pred. No. 76; 0; Mismatches
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                                                                        protein.
1BCACBAB4752B316 CRC64;
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            DB . 76;
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WREDLINE-2238/257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

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A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Halakesley R.W., Touchman J.W., Green E.J., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                    Query Match
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Matches 7
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Q6ING9;
05-JUL-2004 (TrEMB)
05-JUL-2004 (TrEMB)
05-JUL-2004 (TREMB)
MGC82621 protein.
Name=MGC82621;
                                                                                                                                                                                                                                                                                                  SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-I-SIMILARITY: Belongs to the PP2C family.
EMBL; BC072112; AAH72312.1; -.
InterPro; IPR0019212; PP2C.
InterPro; IPR001932; PP2C-1ike.
PF6m; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.; "Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                              Hydrolase; Magnesium. seQUENCE 373 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S.L., St
Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-22341132; PubMed-12454917;
                                                          29
                                                                                                                    Similarity 7; Conser
                                                          PERKEEK 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.L., Wagner L.,
                                                                                                                    17.1%; Score 7; DB (larity 100.0%; Pred. No. 83) Conservative 0; Mismatches
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XX Klausner R.D., Collins F.S., Wagner L., Shenfer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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XX Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altschenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheet T.E.,

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XX Altschenko L., Marusina K., Bonaldo M.F., Casavant T.L., Prange C.,

XX Altschenko L., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Altschenko L., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Altschenko L., M.C., Peters G.J., Abrameon R.D., Mullahy S.J.,

XX Altschenko L., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Altschenko L., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Altschenko L., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Altschenko L., McLaus A., Fother B.D., Dickson M.C.,

XX Altschenko L., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Alches S. J. Marra M.A.
                                                                       Matches
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Best Local
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Submitted (JUN-2004) to the
EMBL; BC072312; AAH72312.1;
Hypothetical protein.
SEQUENCE 373 AA; 41536 MY
                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Klain S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Abm74402 DNA clone	Adq19937 Human sof	Abp64856 Human pro	Aaw48812 Human KDE	Aag59937 Arabidops	Aag07744 Arabidops	Adn74077 Thale cre	Aag07745 Arabidops	Aag59938 Arabidops	Aay22570 Bacterial		Aag59939 Arabidops	Adk48744 Streptoco	Abu01034 S. pneumo	Ada35306 Acinetoba	Abg22899 Novel hum	Aay52997 Neisseria	Abp38311 Staphyloc	Abm71043 Staphyloc	Aag81563 S. epider

ALIGNMENTS

## RESULT 1 AAB92729 ID AAB92729 ID AAB92729 ID AAB92729 AC AAB9 XX AAB9 XX AAB9 XX Huma 29-JUL-1999; 99JP-00248036. 27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899. Human protein AAB92729; 28-JUL-2000; 2000EP-00116126 EP1074617-A2 Homo sapiens Human; 26-JUN-2001 AAB92729 standard; protein; 07-FEB-2001. (HELI-) HELIX RES INST. primer; Isogai T, Ni: , Sugiyama T, (first entry) sequence SEQ ID NO:11159. detection; diagnosis; antisense therapy; gene therapy. Nishikawa T, T, Wakamatsu 349 ₿ Hayashi K, A, Nagai K, Saito Otsuki Yamamoto

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

WPI; 2001-318749/34.

Ishii S,

., H

Claim 8;

SEQ ID NO 11159;

2537pp + Sequence Listing; English

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Best Local S
Matches 41
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-03726045P.
24-APR-2002; 2002US-0376045P.
                                                                                                                                                         New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynuclectide which comprises a 3'-end sequence, where the oligonuclectide comprises at least 15 nuclectides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13228 and AAH13633 to AAH18742 represent human cDNA sequences; AB954846 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent human cDNAs essent considers, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003054152-A2
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                                                                                                                                                                                                                                                                                                                       2003-569235/53.
DB; ADE07101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 4; 1
100.0%; Pred. No. 4.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue marker; molecular weight marker; disorder.
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The invention proteins. The

comprises the amino acid and DNA and protein sequences of

sequences

coding sequences of novel the invention are useful

Sequence 515

Claim 20;

SEQ ID NO 1078; 1177pp; English.

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                                                                                  The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCAI, binding proteins BARDI, B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a BARDI, B123, BE2, BE14, BE31 or BE445 nucleic acid sequence, specifically a wild type BARDI composition for the detection or purification of BRCAI, useful to identify a patient having, or at risk of developing cancer. BARDI can be used in the preparation of an anti-BARDI antibody, and in the detection and purification of a BRCAI protein. BARDI, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARDI, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARDI, B123, BE2, BE14, BE31 or BE445, a specific anti-BARDI antibody can be used to identify a patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-230317/20.
N-PSDB; AAV24135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 287-288; 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-1996;
03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens BAP28 sequence
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Pred. No. 1.3e-35;
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Query Match

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     Query Match 48.8%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 20; Conservative 0; Mismatches
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                                                                                                                                                          The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polynucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first cDNA sequence of the BAP28 gene consisting of the exons 1 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization oppolymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999; 99US-0141323P.
18-JAN-2000; 2000US-0176880P.
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                                                                                                                 Sequence 2144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 297-304; 349pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barry C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-2000; 2000WO-IB001183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAP28; prostate; tumour; cancer; diagnostic; genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by BAP28
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4e-13;
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Best Local
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14-SEP-1999
          Lactococcus lactis; IL1403
                                                                         29-AUG-2003
16-MAY-2002
                                                                                                                            ABB55123 standard; protein; 453
                                                                                                                                                                                                                                                                     Sequence 220 AA;
                                                                                                                                                                                                                                                                                        of a microbe, using the gyrase gene as the index. The method involves the use of PCR primers to amplify DNA from the microbe, which is then identified or detected depending on its base sequence. The method can be used to classify and identify an unidentified microbe strain rapidly and with high precision. The present sequence represents a gyrase protein. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23793;
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                              Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                         ABB55123;
                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 14-15; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX86000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitinophaga pinensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                dentification and detection of a microbe
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                                                                                                                                                                                                                           Score 7; DB 2; Pred. No. 24; 0; Mismatches
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ABP60399
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast; HMG-CoA reductase; squalene; zymosterol; cholesta-7,24-dienol; cholesta-5, 7, 24-trienol; zymosterol-24-methyl transferase; ergosta-5, 7, 24 (28)-trienol-22-dehydrogenase; ergosta; dienol; episterol-5-dehydrogenase; linker region; catalytic domain;
                    Mukharji I,
                                                                                                                                                                                                                                                   24-OCT-1995.
                                                                                                                                                                                                                                                                                                                                                          Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at
                                                                                                                                  15-NOV-1990;
                                                                                                                                                                                          28-OCT-1991;
                                                                                                                                                                                                                                                                                                           US5460949-A.
                                                                                (STAD ) AMOCO
                                                                                                                                                                                                                                                                                                                                                                                                                   membrane binding region; HMG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast HMG2 SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6;
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                    Saunders CA,
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                                                                                CORP
                                                                                                                                                                                                                                                                                                                                                             cerevisiae
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                                                                                                                                  90US-00613380
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100.0%; Pred. No. 46;
tive 0; Mismatches
                    Wolf FR;
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                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme
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14-AUG-1992; 20-SEP-1994.

92US-00934374.

Saccharomyces

US5349126-A

HMG-CoA reductase 2; 3-hydroxy-3-methyl:glutaryl coenzyme A; squalene; sterol.

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RESULT 8
AAR58611
ID AAR5
XX
AC AAR5
XC AAR5
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XC Yeas
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CC zymosterol, Cholesta-7,24-dienol and cholesta-5,7,24-trianol
CC structural gene encoding a polypeptide having HMG-CoA reductase activity
CC in a mutant yeast having defects in the expression of zymosterol-24-
CC (methyl transferase and ergosta-5, 7, 24 (28) -trienol-22-dehydrogenase;
CC (B) a method of increasing squalene, ergosta-8, 22-dienol, ergosta-7, 22-
CC dienol, ergosta-8-enol and ergosta-7-enol accumulation in S. cerevisiae
CC comprising transforming a mutant S.cerevisiae having a defect in the
CC comprising a vector operatively linked to an exogenous DNA segment that
CC comprising a vector operatively linked to an exogenous DNA segment that
CC encodes the catalytic region and at least a portion of the linker region
CC to the free from the membrane binding region of an HMG-CoA reductase
CC enzyme and a promoter suitable for driving the expression of the
CC reductase in the yeast; (C) a method of increasing squalene, zymosterol
CC zymosterol, a promoter transferase and episterol-5-dehydrogenase with a
CC zymosterol, aregosta-5, 7, 24(28)-trienol and ergosta-5, 7-dienol
CC zymosterol, ergosta-5, 7, 24(28)-trienol and ergosta-5, 7-dienol
CC zymosterol, ergosta-5, 7, 24(28)-trienol and ergosta-5, 7-dienol
CC zymosterol, ergosta-5, 7, 24(28)-trienol and ergosta-5, 7-dienol
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                      Yeast HMG-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR58611;
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(HART/) HART E A.
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CC synthase comprising growing several cells in the presence of a conjugation of a conjugation of a conjugation of a conjugation of a conjugation of a conjugation of a conjugation of a conjugation of a conjugation of the cells further comprises at least one isolated and purified nucleic conjugation of a yeast expression library, and the expression of the conjugations where the expression is induced, filtering the cell/resin conjugation of the cell/resin mixture with alcohol to produce an conjugation of the cell/resin mixture with alcohol to produce an conjugation of the cell/resin mixture with alcohol to produce an conjugation of the cell/resin mixture with alcohol to produce an conjugation of the cell/resin mixture with alcohol to produce an conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the c
Sequence 1045 AA;
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                                                                                                seqdata.uspto.gov/sequence.html.
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á Matches Query Match Best Local Local Similarity les 7; Conserv 10 11 HLVKPFA 17 HLVKPFA 16 Conservative 100.0%; 0 Score 7; Pred. No. Mismatches DB 8 5. 97; 8 0 Length 1045; Indels 0 Gaps

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XX OF A Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-COA reductase; enzyme. 01-JUL-2004 ADM98798 standard; protein; HMG-CoA reductase polypeptide #51. (first entry)

Saccharomyces cerevisiae.

US2004072323-A1

15-APR-2004

07-JAN-2002; 2002US-00041018. 05-JAN-2001; 2001US-0259880P

(MATS/) MATSUDA S P T. (HART/) HART E A.

Matsuda SPT, Hart EA;

WPI; 2004-373921/35.

New unicellular organisms comprising exogenous nucleic acids encoding a geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.

Disclosure; SEQ ID NO 218; 38pp; English.

The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence

The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence

Disclosure; SEQ ID NO 199; 38pp; English.

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal; pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.
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New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
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                                                                                                                                                                                                                                                                                   (MATS/) MATSUDA S P T. (HART/) HART E A.
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The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence

precursor

Disclosure; SEQ ID NO

264; 38pp; English

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                          New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal;
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                                                                                                      Disclosure;
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       The invention relates to a unicellular organism or diterpene precursor comprising an exogenous r
                                                                                                                                                                                                                                                                                                           WPI; 2004-373921/35.
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                                                                                                         SEQ ID NO 336; 38pp; English.
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nucleic acid sequence
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CC encoding a geranylgeranyl pyrophosphate synthase under the control of a C promoter operable in the organism, and an exogenous nucleic acid sequence cencoding a diterpene synthase under the control of a promoter operable in CC the organism. The invention also relates to methods of producing a CC diterpene or diterpene precursor and a method of isolating a diterpene comprising growing several cells in the presence of a cC golyaromatic resin to make a cell/resin mixture, where at least one of CC the cells further comprises at least one isolated and purified nucleic acid sequence of a yeast expression library, and the expression of the cull-resin expression is inducible promoter under comprise at the expression is inducible promoter under conditions where the expression is induced, filtering the cell/resin corganic eluent and analysing the organic eluent by a screening method corganic eluent and analysing the organic eluent by a screening method corganic eluent and analysing the organic eluent by a screening method corganic eluent and analysing the organic eluent by a screening method corganic eluent and setting the organic eluent by a screening method corganic eluent and salidate eluent by a screening method corganic eluent and salidate eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent eluent elle ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ellente ell
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Best Local
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New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
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The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

Claim 27; SEQ ID NO 26531; 487pp; English

Disclosure; SEQ ID NO 309; 38pp; English

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RESULT 14
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21-SEP-2000;
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26-MAY-2000;
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2000US-0236359P.
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                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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26-MAY-2000;
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Sequence 51 AA;
                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 36707; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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1: uniprot_sprot:*
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1 LKGLFTLFAGHLVKPFADTL.....QVNISKTDEAFFDSENDPEK 41
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Q7RDU5
Q87P73
Q9KSB9
Q9KSB9
Q9KSB9
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakanatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Isono Y., Nakamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Yaku Y., Kodaira H., Kondo H.,
RA Omura Y., Abe K., Kamihara K., Katuuta N., Sato K., Tanikawa K.,
RA Omura Y., Abe K., Kamihara K., Katuuta N., Sato K., Tanikawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujinori K., Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Yoshikawa Y., Matsunawa H., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yujinori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Takhashi Y., Nakagawa K.,
RA Nomira K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
CDMAs., "Sasaki M., Watanabe M., Kikuchi H., Masuho Y., Yamashita R.,
CDMAs., "Sasaki M., Nakajima Y., Mizuno T., Takhashi Y., Nakagawa K.,
RA Nakai K., Nakajima M., Taki K., Mizuno S., Sugano S.;
CDMAs
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EMBL; AK001221; BAA91564.1; ALT_INIT.
                                                        InterPro; IPR008938; ARM.
InterPro; IPR008937; HEAT.
InterPro; IPR000357; HEAT_REPEAT; FALSE_NEG.
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-!- SIMILARITY: Belongs to the BAP28 family.
-!- SIMILARITY: Contains 1 HEAT repeat.
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Ota T., Suzuki Y., Nishikawa T., Ots
Wakamatsu A., Hayashi K., Sato H., N
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"A novel BAP28 gene and protein.";
Patent number WO0100669, 04-JAN-2001.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ery Match	Octobrass School	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SETRAIN=mix FYB/N; TISSUE=Mammary tumor. WAP-TGF alpha MEDLINE=22388257; PubMeda12477932; Strausberg R.L., Peingold E.A., Grou Klausner R.D., Collins F.S., Wagner Altschul S.F., Zeeberg B., Buetow K. HOpkins R.F., Jordan H., Moore T., M Diatchenko L., Marusina K., Farmer A Stapleton M., Soares M.B., Bonaldo M Brownstein M.J., Usdin T.B., Toshiyu Raha S.S., Loquellano N.A., Peters G Bosak S.A., McEwan P.J., McKernan K. Richards S., Worley K.C., Hale S., G Villalon D.K., Muzny D.M., Sodergren Rahey J., Helton E., Ketteman M., Man Whiting M., Madan A., Young A.C., Sh Blakesley R. M., Touchman J. W., Green Rodriguez A.C., Grimwood J., Schmutz Krzywinski M.I., Skalska U., Smailus Jones S.J., Marra M.A.; "Generation and initial analysis of 1 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:168	ILT 3  WI Q8VCK1 Q8VCK1 Q8VCK1 Q1-MAR-2002 (TIEMBL 01-MAR-2002 (TIEMBL 01-MAR-2004 (TIEMBL BC019693 protein. Name=BC019693, Name=BC019693, Mus musculus (Mouse Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;	Query Match Best Local Si Matches 41; Y 1 L y 1 1947 L	VARIANT VARIANT VARIANT VARIANT SEQUENCE
nilarity	ENCE FROM N.A. ILIN=mix.FVB/N; IUS=Mammary tumor. IUS=Mammary tumor. ILIN=mix.FVB/N; ILIN=mix.	FROM N.A.  X FYBIN  mmmary tumor. WAP  2388257; PubMeda  R.D., Feingold  R.D., Collins  S.F., Zeeberg B.  S.F., Jordan H.,  O.L., Marusina H.,  M., Soares M.B.  M., Soares M.B.  M., Godellano N.A.  M.CEWAN P.J.,  S., Worley K.C.,  Morley K.C.,  Morley K.C.,  Morley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  S., Worley K.C.,  Morley K.C.,  J., Walshan  J., Keth  M.I., Skalska	PRELIMINARY,  2 (TrEMBLrel.  2 (TrEMBLrel.  7 (TrEMBLrel.  603;  1693;  108 (Mouse).  108 (Mouse).	imilarity Conserv LKGLFTLFAC	1694 1 1854 1 1967 1 2017 2 2144 AA;
87.8%; 100.0%;	N.A.  (N);  (Tumor. WAP-TGF  (Tumor. WAP-TGF  (A)  (A)  (A)  (B)  (B)  (B)  (B)  (B)	FROM N.A.  FYB/N;  X FYB/N;  X FYB/N;  RD, Collins F.S., Wagner  S.F., Zeeberg B., Buetow K.  F., Jordan H., Moore T., N  O L., Marusina K., Farmer J.  M., Soares M.B., Bonaldo N.  I. Loquellano N.A., Peters K.  M., Wardellano N.A., Peters K.  M., Muzny D. M., Sodergrer  Helton E., Ketteman M., Marusina K., Farmer J.  R. W., Touwond J.W., Greer  Helton E., Ketteman M., S.  R. W., Touwond J.W., Greer  A.C., Grimwood J., Schmutz  i M.I., Skalska U., Smailuu  on and initial analysis of  cDNA sequences.";  1. Acad. Sci. U.S.A. 99:168	INARY;  Lirel. 20, Li  Lirel. 26, Li  Chordata;  Rodentia;	100.0%; Y 100.0%; EVATIVE AGHLVKPFADT AGHLVKPFADT	1694 1854 1967 2017 2017
Score 36; DB 2; Pred. No. 2.5e-29	<pre>3F alpha model. 7 m EMBL/GenBank/DDBJ 1; 9763D0331AD0F51</pre>	model.  E. C. L.  H. Sc  Ax S.I  Ax S.	PRT; 349 AA. Created) Last sequence update) Last annotation update) a; Craniata; Vertebrata; a; Sciurognathi; Muridae	Score 41; DB 1; Pred. No. 6.1e-34; 0; Mismatches 0; LNQVNISKTDEAFFDSENDP	N -> S. /FTId=VAR_010939. V -> A. /FTId=VAR_010940. N -> D. /FTId=VAR_010941. E -> G. /FTId=VAR_010942. MW; D66815EE78D8C9
Length 349;	onths old; databases. 5 CRC64;	7 months old; Derge J.G., Berge J.G., haefer C.F., Bhat N.K., haefer C.F., Bhat N.K., Wang J., Hsieh F., ubin G.M., Hong L., asavant T.L., Scheetz T.E., Carninci P., Prange C., Carninci P., Prange C., D., Mullahy S.J., bramson R.D., Mullahy S.J., lek J.A., Gounaratne P.H., lek J.A., Gunaratne P.H., Lu X., Gibbs R.A., Lu X., Gibbs R.A., ko Y., Bouffard G.G., Dickson M.C., Rodrigues S., Sanchez A., ko Y., Bouffard G.G., Schnerch A., Schein J.E., han 15,000 full-length human 03(2002).	te) te, ta, Euteleostomi, dae, Murinae, Mus.	Length 2144; Indels . 0; Gaps EK 41	B7 CRC64;
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LKGLFTLFAGHLVKPFADTLNQVNISKTDEAFFDSE 187 

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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Olfactory brain;
STRAIN-C57BL/6J; TISSUE-Olfactory brain;
STRAIN-C57BL/6J; TISSUE-Olfactory brain;
Adachi J., Aizawa K., Akimura T., Arakawa T., Hashizume W.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T.,
Hayashida K., Hayatsu N., Hiramoto K., Kisawa I., Kasukawa T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya
Katoh H., Kawai J., Kojima Y., Miyazaki A., Murata M., Nakamura M.,
                                                                                                                                                                                                           STRAIN-C57BL/63; TISSUE-Olfactory brain;

STRAIN-C57BL/63; TISSUE-Olfactory brain;

STRAIN-C57BL/63; TISSUE-Olfactory brain;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN Integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:643040006 product:hypothetical ARM repeat
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STRAIN-C57EL/63; TISSUE-Olfactory brain;
STRAIN-C578L/63; TISSUE-1042159;
MEDLINE-20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatu M., Hayashizaki Y.,
Konno H., Okazaki Y., Muramatu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
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STRAIN-C57BL/6J; TISSUE-Olfactory brain;
MEDLINE-21085660; PubMed-11217851;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Olfactory brain.
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STRAIN-C57BL/6J; TISSUE-Olfactory
MEDLINE-99279253; PubMed-10349636;
Carninci P., Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Team;
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hgieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hgieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hgieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Schaetz T.E.,

A Hopkins R.F., Jordan R., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Biskards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Korpen S. T. Marra M.A., Schmutz J., Myers R.M., Butterfield Y.S.,

Korpen S. T. Marra M.A., Schmutz J., Schmerch A., Schein J.E.,

Jones S. T. Marra M.A., Schmutz J., Schmerch A., Schein J.E.,

Jones S. T. Marra M.A., Schmutz J., Schmerch A., Schein J.E.,

Jones S. T. Marra M.A., Schmutz J., Schmerch A., Schein J.E.,

Jones S. T. Marra M.A., Schmutz J., Schmerch A., Schein J.E.,

Jones S. T. Marra M.A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Sch
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01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                               InterPro;
SEQUENCE
                                                                                                    Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC011983; AAH11983.1; -.
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Mammalia; Eutheria;
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Name=FLJ10359;
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                                                                                                                                                                                                                                  "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SEQUENCE 40
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                    Score 20;
Pred. No.
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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Twyanagi T., Wagateuma M., Shiratori A.,
RA Murakami K., Yasuda T., Twyanagi T., Wagateuma M., Shiratori A.,
RA Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kirkawa K., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tarikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Cono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Asaehori K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Fujinori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamra Y., Ohara O., Isogai T., Sugano S.,
RT Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 20
                                                                                                          Q6P197;
Q6P197;
 Homo
                   FLJ10359 protein (Fragment).
Name=FLJ10359;
                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, La
01-OCT-2003 (TrEMBLrel. 25, La
01-OCT-2003 (TrEMBLrel. 25, La
Hypothetical protein FLJ40893.
Homo sapiens (Human)
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Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local
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TISSUE-Lymph;

TISSUE-Lymph;

TISSUE-Lymph;

TISSUE-Lymph;

MEDLINE-2238857; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
FLJ10359 protein (Fragme
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Mammalia; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH65205
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PibMed=12477932;
MEDLINE=22388257; PibMed=12477932;
MEDLINE=27388257; PibMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generation and initial analysis and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Primates;
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27,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Shenmen C.M., Schuler G.D.
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Best Local
                                                                                      InterPro; IPR003945; NADHDL oxred5.
InterPro; IPR003916; NADHND oxred5.
InterPro; IPR001750; Oxidored q1.
InterPro; IPR001218; Oxidored q1_C.
InterPro; IPR001516; Oxidored q1_C.
InterPro; IPR001516; Oxidored q1_C.
Pfam; PF00361; Oxidored q1_C; 1.
Pfam; PF001010; Oxidored q1_C; 1.
Pfam; PF010104; Oxidored q1_C; 1.
Pfam; PF010435; Oxidored q1_C; 1.
Pfam; PF010435; NP0XDRDTASE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ431206; CAD24024.1; -.
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0009523; C:photosystem II; IEA.
GO; GO:0009523; C:photosystem II; IEA.
GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; P:ATP synthesis coupled electron transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Montiniaceae; Kaliphora.
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submitted (JAN-2004) to the
EMBL; BC065205; AAH65205.1;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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TIGRO1974; NDH_I L; 1.
st; NAD; NADP; OxIdoreductase; Plastoquinone; Quinone.
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Best Local S
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GO; GO:0006955; P:immune response; IEA.

RINterPro; IPR0077110; Ig-like.

RINterPro; IPR003597; Ig-cl.

RINterPro; IPR003006; Ig-MHC.

RINterPro; IPR003006; Ig-MHC.

RINterPro; IPR003006; Ig-MHC.

RINterPro; IPR003006; Ig-MHC.

RINTERPO7654; Cl-set; 1.

R Pfam; PF07654; Cl-set; 1.

R Pfam; PF00993; MHC_II_alpha; 1.

R Pfam; PF00993; IG-LIKE; 1.

R PROSITE; PS003290; IG-MHC; UNKNOWN 1.

R PROSITE; PS003290; IG-MHC; UNKNOWN 1.

SEQUENCE 236 AA; Z6312 MW; 8C8DAB02C4CE827B CRC64;
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Best Local
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Q81DM8;
01-JUN-2003
                                                          ORFNames=BC2329;
Bacillus cereus (strain
Bacteria; Firmicutes; Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "MHC class II A genes in the channel Dev. Comp. Immunol. 24:609-622(2000) EMBL; AF103003; AAD19866.1; -. EMBL; AF103002; AAD19865.1; -. HSSP; P28068; IHDM.
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MEDLINE=20292992; PubMed=10831795;
MEDLINE=70292992; PubMed=10831795;
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01-OCT-2003
                             NCBI_TaxID=226900;
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Clem L.W., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinopterygii; Neopterygii; Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata;
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SEQUENCE FROM N.A.
                                                                                                                            Zinc uptake transporter.
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697 AA;
                                                                                                                                                (TrEMBLrel.
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                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                               68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                               in ATCC 14579 / DSM 31).
Bacillales; Bacillaceae;
                                                                                                                                                24,
25,
                                                                                                                                              Last sequence up
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DB . 47;
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                                                               Bacillus
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RESULT 12
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Q87Z92;
Q1-JUN-2003
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Overbeek R., Kyrpides N.C.;
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                                                                                                                                                                                                                    "The complete genome sequence of the Arabidopsis and Pseudomonas syringae pv. tomato DC3000."; Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
                                                                                                                                                                                                                                                           Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwinn M.L., Doddson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
Nelson W.C., Davidsen T.M., Zaffar N., Zhou L., Liu J., Yuan Q.,
Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A
Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang
Bender C.L., White O., Fraser C.M., Collmer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Bacterial transferase, hexapeptide repeat protein.
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Kapatral V.,
                                                                                                            SEQUENCE
                                                                                                                                                                                          EMBL; AE016868; AA057013.1; -. TIGR; PSPTO3538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=PSPTO3538;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0046873; F:metal ion transporter activity;
GO; GO:0030001; P:metal ion transport; IEA.
InterPro; IPR003689; Zn_transpt_Zip.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
                                                                                                                                      Pfam; PF00132; Hexapep;
                                                                                                                                                GO; GO:0016740; F:transferase activity;
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR011004; Trimer_LpxA_like.
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 266
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7; Conserv
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                                                    Similarity 7; Conser
 KGLFTLF 272
                           KGLFTLF 8
                                                                                                                      proteome;
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245 AA;
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                                                       Conservative
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tacharyya A., Reznik G., Mikhailova N., Lapidus
Galtsman E., Larsen N., D'Souza M., Walunas T.,
h G., Haselkorn R., Fonstein M., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas.
                                                                                                                         Transferase.
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100.0%;
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100.0%; Pred. No.
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No.
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                                                                    DB 2;
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                                                                               Length 273;
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                                                                                                              CRC64;
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RESULT
Q9AAU6
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01-JUN-2001
01-JUN-2001
01-MAR-2004
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SEQUENCE
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STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermoleeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
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Q8HS77;
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OrderedLocusNames=CC0498;
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                                                                                                                                                         Oceanopapaver within Tiliaceae).";
                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosideurosids II; Malvales; Malvaceae; Grewioideae; Corchorus.
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
Whitlock B.A., Karol K.G.,
"Chloroplast DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EWBL; AE005722; AAK22485.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M.;
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                                                                                                               EMBL;
                                                                                                                                    Int. J. Plant Sci. 164:35-41(2003).
                                                                                                                                                                                                                                                                                    NCBI_TaxID=210143;
                                                                                                                                                                                                                                                                                                                                                                                                        Corchorus capsularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ndhF;
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BL; AF523838; GO:0009507; GO:0009523; GO:0008137; GO:0016491; GO:0042773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
AAO16032.1; -. C:chloroplast; IEA.
C:photosystem II; IEA.
C:photosystem II; IEA.
F:NADH dehydrogenase (ubiquinone) activity;
F:oxidoreductase activity; IEA.
P:ATP synthesis coupled electron transport;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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RESULT 15
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.,
                                                                                                                                                                                                                          EMBL; AABLO1001679; EAA17333.1; -.
Hypothetical protein.
SEQUENCE 367 AA; 42633 MW; F6C
                                                                                                                                                                                                                                                                                                                                        "Genome sequence and comparative analysis of the model rodent malaria parasite plasmodium yoelii yoelii.";
Nature 419:512-519(2002).

-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is prolificary ALDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium yoʻelii yoʻelii.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. Name=PY05325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTRDUS;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=17XNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=12368865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 17.1%; Score 7; DB 2; Local Similarity 100.0%; Pred. No. 67; 198 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                     preliminary data.
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229 LFTLFAG 235
226 NOVNISK 232
                                                   21 NOVNISK 27
                                                                                                             Similarity 7; Conserv
                                                                                                                   Conservative
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                                                                                                                                                                                                                                42633 MW; F6C1CD4DB0636487 CRC64;
                                                                                                       17.1%; Score 7; DB 2
100.0%; Pred. No. 68;
tive 0; Mismatches
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                                                                                                                                           DB 2;
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Search completed: February 1, 2005, 15:31:04 Job time: 70.5556 secs

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Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Maximum
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US-09-879-957-79
US-09-879-957-79
US-09-134-001C-3156
US-09-134-001C-3156
US-09-138-352-6593
US-09-270-767-61729
US-09-270-767-61729
US-09-270-767-47614
US-09-270-767-47614
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US-09-133-735-1
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US-09-489-039A-2794
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Sequence 4, Appli
Sequence 40, Appl
Sequence 61729, A
Sequence 32397, A
Sequence 7614, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 3203, Ap
Sequence 8175, Ap
Sequence 12794, A
Sequence 12794, A
Sequence 128963, A
Sequence 5098, Ap
Sequence 5098, Ap
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31479, A
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	29884, A	4, Appli	17535, A	2, Appli	3675, Ap	46168, A	6, Appli	18781, A	4, Appli	4, Appli	851, App	18, Appl	19, Appl	213, App	18880, A	7644, Ap	8708, Ap	1000

## ALIGNMENTS

GENERAL INFORMATION:

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Sequence 6, Application US/09823823 Patent No. 6635904

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US-09-252-991A-31479
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Sequence 31479, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

FULE RETERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
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Best Local S
Matches 7
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LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yamamoto, Satoshi
APPLICANT: Kasai, Hiroaki
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Suzuki, Makoto
APPLICANT: Hamoda, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING
TITLE OF INVENTION: GENE AS AN INDICATOR
FILE REFERENCE: 12817-004001
CURRENT FAPLICATION NUMBER: US/09/823,823
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/208,688
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 97/343316 PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Chitinophaga pinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ses 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                        130 SENDPEK 136
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100.0%; Pred. No.
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US-07-934-374-6
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HOLECULE TYPE: protein
US-07-596-467-6
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Best Local Similarity
Watches 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31479
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             Sequence 6, Application US/07934374
Patent No. 5349126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           NAME: Gamson, Edward P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 616-5400
TELEPAX: 312 616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-07-2
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31479
LENGTH: 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cuellar, R.
APPLICANT: Wolf, Fred R.
TITLE OF INVENTION: Method and Composition for Increasing
TITLE OF INVENTION: Sterol Accumulation in Higher Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US
FILING DATE: 19901012
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: 1
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STATE: Illinois
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Chappell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chappell, J.
Saunders, Court A.
Cuellar, R.
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                  17.1%; Score 7; DB 1
100.0%; Pred. No. 22;
tive 0; Mismatches
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100.0%; Pred. No.
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o. 12;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TELEPAX: 312 616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 amino acids
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,374
FILING DATE: 19920814
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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APPLICANT: Cuellar, R.
APPLICANT: Wolf, Fred R.
TITLE OF INVENTION: Process and Composition for Increasing
TITLE OF INVENTION: Sterol Accumulation in Higher Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
APPLICATION NUMBER: UPFILING DATE: 19911028 CLASSIFICATION: 435
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                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 HLVKPFA 17
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GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/07783861C
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                                                                                                                                                                                                                                    E: Amoco Corp., Patents and Licensing Dept
200 East Randolph St.
                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                             Wolf, Fred R.
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                                                                                                                                                                                                                                                                                                                                                                                                     Saunders, Court A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dressler, Goldsmith, Shore, Sutker & Milnamow
                                                                                                                                                                                                                                                                                                                            A Method and Composition for Increasing the Accumulation of Squalene and Specific Sterols in
                                                                                                                                                                                                                                                                                                               Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.1%; Score 7; DB 1; 100.0%; Pred. No. 22;
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                                US/07/783,861C
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

15-NOV-1990

US 07/613,380

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US-08-630-915A-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNY AGENT INFORMATION:

NAME: Galloway, No. 5460949vall B.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312 856-7180

TELEFAX: 312 856-7180

TELEFAX: 312 856-4972

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1045 amino acids

TYPE: AMINO ACID

TYPE: AMINO ACID
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                        TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HOPFMAN,
APPLICANT: KAY, Brid
APPLICANT: FOWLKES,
APPLICANT: WCCONNELL
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MJSTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                          STRANDEDNESS
                                                                                                                                                                                     TELEPHONE: (214/ / 1974)
TELEPHONE: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                           TOPOLOGY:
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                                                                                                                              ENGTH:
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                                                                                                           amino acid
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                                                                                                                              41 amino acids
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TVENTION: POLYBEPTIDES HAVING A FUNCTIONAL
TVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOFFMAN, No. 6309820h
KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.1%; Score 7; DB:
larity 100.0%; Pred. No. 22.
Conservative 0; Mismatches
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                                                                           unknown
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                                                      peptide
 14.6%; Score 6;
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 DB 3;
Length 41;
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GENERAL INFORMATION:

Sequence 7883, Application US/09543681A Patent No. 6605709

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TOPOLOGY: unknown;

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-879-957-79
                                                                                                                                  Query Match
Best Local Similarity
Tatches 6; Conserv
RESULT 8
US-09-543-681A-7883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-879-957-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 79, Applicati Patent No. 6709821 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 79: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 118/872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USING SAME
NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SPARKS, Andrew B. HOFFMAN, No. 6709821h
                                                                            29 ENDPEK 34
                                                                                                                36 ENDPEK 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                       LENGTH: 41 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09879957
                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAY, Brian K.
                                                                                                                                                 14.6%; Score 6; DB . 100.0%; Pred. No. 11 tive 0; Mismatches
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                                                                                                                                                                         DB 4;
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APPLICANT: GARY BRETON

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APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Dro

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILLING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 61018

LENGTH: 70

TYPE: PRT

ORGANISM: Drosophila melanogaster
FEARTURE:

ORGANISM: Drosophila melanogaster
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-61018
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US-09-270-767-61018
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US-09-543-681A-7883
                                                                                           PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 220
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 7883
                                                                                                                                                                                                                                                                                                       Sequence 220, Application US/09710279
Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
OTHER INFORMATION: Description of Artificial Sequence: synthetic
                                     ORGANISM: Artificial Sequence
                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 65
TYPE: PRT
                                                                             ENGTH: 120
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US-09-673-898-10
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Best Local Similarity
"---hes 6; Conserv?
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                                                                                                                       US-09-673-898-10
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US-09-134-001C-3156
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                                                                                                                                                NUMBER OF SEQ ID NOS: 16
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 129
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3156
LENGTH: 121
TYPE: PRT
                                                          Matches
                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                              Patent No. 6709657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/673,898
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: PCT/EP99/02765
PRIOR FILING DATE: 1999-04-20
                                                                                                                                                                                                                                                                                    APPLICANT: Ruelle, Jean Louis
TITLE OF INVENTION: BASBO13 DNA AND PROTEINS FROM NEISSERIA
TITLE OF INVENTION: MENINGITIDIS
FILE REFERENCE: BM45307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                   ORGANISM: Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 6; Conserv
 31
                            26 SKTDEA 31
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                                                          Similarity 6; Conserv
SKTDEA 36
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                                                           Conservative
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                                                                        Score 6;
Pred. No.
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Pred. No.
                                                           Mismatches
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33;
                                                                        DB 4;
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                                                                                    Length 129
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; MOLECULE TYPE: protein US-08-698-805-4
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TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-328-352-6593
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6593, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/698,805
FILING DATE: 16-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,510
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chapman, Ma:
APPLICANT: Arruda, L. I
TITLE OF INVENTION: Mo:
TITLE OF INVENTION: And
TITLE OF INVENTION: And
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC DOS/MS-DOS
OPTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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Local Similarity 100.0%; Pred. No. 44;
hes 6; Conservative 0; Mismatches
                                                           TYPE: amino acids
                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LVKPFA 126
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                                                                                                                                                   703-413-2220
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Molecular Cloning of Cockroach
Allergens, Amino Acid and Nucleotide Sequences Therefore,
and Recombinant Expression Thereof
                                                                                                                                                                                                              494-203-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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Search completed: February 1,

2005, 15:35:44

: 18.5556 secs

Job time

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APPLICANT: Youngman, FRILLY
APPLICANT: Fritz, Chrisian
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
FILLE REFERENCE: 07334/060001
CURRENT APPLICATION NUMBER: US/09/222,938A
CURRENT FILING DATE: 1998-12-30
INUMBER OF SEQ ID NOS: 102
SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 40
SEQ ID NO 40
ILENGTH: 200
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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                                                            Best Local Similarity
Matches 6; Conserv
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                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                         Sequence 40, Application US/09222938A Patent No. 6437108
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Best Local Similarity
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121 QVNISK 126
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0; Mismatches
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Maximum DB seq length: 2000000000
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11111111111111111111111111111111111111	Result No.
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17. 1 17. 1 17. 1 17. 1 17. 1 17. 1 14. 6	Query Match
10445 10445 10445 10445 10445 10445 10445	Query Match Length DB
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US-10-43-963-193489 US-09-823-829-6 US-09-823-823-6 US-10-369-493-1836 US-10-041-018-199 US-10-041-018-218 US-10-041-018-309 US-10-041-018-309 US-10-041-018-36 US-10-041-018-36 US-10-041-018-36 US-10-041-018-36 US-10-041-018-36 US-09-864-761-34609	ID
Sequence 103, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1835, Ap Sequence 199, App Sequence 218, App Sequence 264, App Sequence 309, App Sequence 336, App Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl	Description

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15	17	14	14	14	9	9	17	17	17	16	16	16	15	15	15	17	15	25	15	16	16	15	15	17	17	15	17	16	16	15	9
-424-599-14835	-10-425-115-	212-872-	US-10-074-095-461	-10-079-854-	09-764-860-4	764-	-10-425-115-34227	-10-425-	-10-425-115-19883	US-10-739-956-10	-10-767-701-	-10-437-963-11401	-10-424-599-17	US-10-041-018-351	US-10-041-018-211	-10-425-115	-10-424-599-24415	-10-424-599-1	-10-424-599-2	-10-767-701-	37-963-	-10-424-599-18275	-10-424-599-	-25058	-10-425-115-	US-10-424-599-143186	-425-115-2776	-767-701-	-10-437-963-1049	-599-284	US-09-864-761-47882
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# ALIGNMENTS

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5	PRIOR APPLICATION NUMBER: PCT/US01/03800  PRIOR FILLING DATE: 2001-02-05	 PRIOR APPLICATION NUMBER: US 09/496,914 PRIOR FILING DATE: 2000-02-03		FILING DATE	PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: US 09/491,404	-		DRIOR ADDITION NIMBER: IS 04/552 317	-	PRIOR FILING DATE: 2001-12-11	PRIOR APPLICATION NUMBER: US 60/339,453	CURRENT FILING DATE: 2002-04-22	CURRENT APPLICATION NUMBER: US/10/128.558	TITLE OF INVENTION: Polypeptides	TITLE OF INVENTION: Novel Nucleic Acids and	APPLICANT: Drmanac, Radoje T	APPLICANT: Boyle, Bryan J		APPLICANT: Wang, Zhiwei	APPLICANT: Tang, Y. Tom	GENERAL INFORMATION:		Sequence 167, Application US/10128558	RESULT 1 US-10-128-558-167

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US-10-128-558-167
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                                                                                                                                                                                                                             Sequence 6, Application US/09823829 Patent No. US20020146697A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
       APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Kasai, Hiroaki
APPLICANT: Hamada, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR FILE REFERENCE: 12817-004001
CURRENT APPLICATION NUMBER: US/09/823,829
CURRENT FILING DATE: 2001-03-30
CURRENT FILING DATE: 2001-03-30
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Best Local Similarity
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SOFTWARE: pt FL genes Version 6.0
SEQ ID NO 167
LENGTH: 1149
PRIOR APPLICATION NUMBER: US 09/208,688
                                                                                                                                                 APPLICANT: Yamamoto, Satoshi
APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 193489, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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NAME/KEY: unsure
LOCATION: (1)..(182)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT4530_89622C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Wei
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100.0%; Pred. No. 6.8e-12;
ative 0; Mismatches 0;
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
FITTE OF INVENTION: FLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/823,823
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/208,688
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: JP 97/343316
PRIOR PILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN VETSION 2.0
SEQ ID NO 6
SEQ ID NO 6
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Best Local Similarity
Watches 7; Conserve
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TYPB: PRT
; ORGANIEM: Chitinophaga pinensis
US-09-823-829-6
                                                                                                                                                                                                                                                          Sequence 1836, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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APPLICANT: Kasai, Hiroaki
APPLICANT: Nakamura, Shoko
APPLICANT: Nukamura, Shoko
APPLICANT: Suzuki; Makoto
APPLICANT: Hamoda, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GY
TITLE OF INVENTION: GENE AS AN INDICATOR
FILE REFERENCE: 12817-004001
FILE REFERENCE: 12817-004001
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PRIOR APPLICATION NUMBER: JP
PRIOR FILING DATE: 1997-12-12
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Pred. No.
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APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILLING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.1
SEQ ID NO 199
LENGTH: 1045
TYPE: PRT
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SEQ ID NO 1836
LENGTH: 1045
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SEQ ID NO 218
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Best Local
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                                                                                                                                                                                                                                       APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
PILE REFERENCE: P02080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 413
                                                                                                                                  TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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11 HLVKPFA 17
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                                                  Similarity
7; Conserv
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                                                17.1%; Score 7; DB 15; L
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No.
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o. 1.6e+02;
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US-10-041-018-264
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US-10-041-018-336
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                 Sequence 336, Application US/10041018
Publication No. US20040072323A1
GRMERAL INFORMATION:
APPLICANT: Matsuda, Seitchi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.1
SEQ ID NO 309
LENGTH: 1045
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Mateuda, Seiichi P.T.
APPLICANT: Matt, Elizabeth A.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080USI/10025547
FILE REFERENCE: P02080USI/10025547
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APPLICANT: Hart, Elizabeth A.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
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CURRENT FILING DATE: 2002-01-07
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CURRENT APPLICATION NUMBER: US/10/041,018
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Pred. No.
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o. 1.6e+02;
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; TOPOLOGY: unknown CLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: 5 US-09-879-957-79
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PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.1
SEQ ID NO 336
LENGTH: 1045
TYPE: PRT
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Best Local Similarity
Watches 7; Conserva
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US-09-879-957-79
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                       Query Match
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Patent No. US200200347
GENERAL INFORMATION:
APPLICANT: SPAR
                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 79: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE, DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
PILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                             LENGTH: 41 amino acids
                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                NAME: Misrock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09879957
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FOWLKES, Dana M.
MCCONNELL, Stephe
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HOFFMAN, No. US20020034755A1h
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                                                                                                                                                                                                                                        (212)
 14.6%;
100.0%;
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100.0%; Pred. No. 1.{
ative 0; Mismatches
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                                                                       SEQ ID NO:
Score 6; DB 9;
Pred. No. 89;
                                                                       79:
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             Length 41;
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Best Local Similarity

APPLICANT: Penn, Sharron G.

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; Sequence 34609, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:
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                                                                                                                                                                                    Query Match
Best Local Similarity
Watches 6; Conserve
                                                     US-09-864-761-34609
                                                                          RESULT 13
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                                                                                                                                                                                                                                                                             US-10-807-856-79
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US-10-807-856-79
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INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
SPICATION UMMBER: US/10/807,856
FILING DATE: 23-Msr-2004
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 227
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                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
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FOWLKES, Dana M.
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Best Local S
Matches 6
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SEQ ID NO 34609
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OTHER INFORMATION: MOTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 45
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR PPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR APPLICATION NUMBER: PCT/US01/00667
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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Then, Wensheng
DTLDQV 14
                                     DTLDQV 23
                                                                            14.6%; Score 6; DB ! llarity 100.0%; Pred. No. 97 Conservative 0; Mismatches
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ED IN HELLO, SIGNAL = 3.8
ED IN HELA, SIGNAL = 4.8
ED IN HEART, SIGNAL = 9.8
ED IN LUNG, SIGNAL = 1.3
ED IN BONE MARROW, SIGNAL = 1.7
ED IN BRAIN, SIGNAL = 4.2
ED IN BRAIN, SIGNAL = 4.2
ED IN BT474, SIGNAL = 4.1
ED IN FETAL LIVER, SIGNAL = 2.4
ED IN FETAL LIVER, SIGNAL = 2.1
ED IN FETAL LIVER, SIGNAL = 2.1
ED IN FETAL LIVER, SIGNAL = 2.1
ED IN FETAL LIVER, SIGNAL = 2.1
                                                                                                                                                                                     AW614813.1, EVALUE 3.00e-19
                                                                                                  DB 9;
                                                                                                                     Length 45;
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; OTHER INFORMATION: MAP TO AC008897.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: SWISSPROT HIT: P04035, EVALUE 6.00e-24
US-09-864-761-47882
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PRILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00665
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US-09-864-761-47882
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SEQ ID NO 47882
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                             Matches
                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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  AGHLVK 14
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Hanzel, David K.
Chen, Wensheng
                                                       14.6%; Sillarity 100.0%; I Conservative 0;
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: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listing Engine vers.
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                                                             Score 6; DB 9; Pred. No. 1.1
                                                                                      DB 9; Le
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                                                                                                               Length 51;
                                                                   Indels
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RESULT 15
US-10-424-599-284582
US-10-424-599-284582
Sequence 284582, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
VIMMEER OF SEQ ID NOS: 285684
SEQ ID NO 284582
LENGTH: 55
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_99002C.1.pep
US-10-424-599-284582
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Search completed: February 1, 2005, 15:44:50 Job time: 61.7778 secs
                                                                                                                                                                                        Query Match 14.6%; Score 6; DB 15; Length 55; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                             11 HLVKPF 16
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30 HLVKPF 35
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Minimum DB seq length: 21
Maximum DB seq length: 200000000
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Gapop 60.0 , Gapext 60.0
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41
1 LKGLFTLFAGHLVKPFADTL.....QVNISKTDEAFFDSENDPEK 41
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291.016 Million cell updates/sec
                                                                                                                                       283416 seqs, 96216763 residues
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.

Database :

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Post-processing: Listing first 45 summaries

# SUMMARIES

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C; Superfamily: uncharacterized conserved protein

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30
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277	270	263	244	233	231	227	227	227	227	227	226	226	225	225	223
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F82874	AC1781	H70046	T15807	C70128	T32953	A64790	D85555	A90705	F83097	B47080	T35202	G83293	AG2653	C97435	D98060
conserved hypothet	hypothetical prote	probable 3-oxoacyl	hypothetical prote	hypothetical prote	hypothetical prote	probable transcrip	probable 2-compone	probable 2-compone	probable two-compo	transcription acti	probable two-compo	probable two-compo	two component resp	transcription acti	conserved hypothet

# ALIGNMENTS

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hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) II - N/Alternate names: protein L9324.2; protein YLR450w C;Species: Saccharomyces cerevisiae C.Pate: 28-Feb-1990 #sequence revision 28-Feb-1990 #tex C;Accession: B30239; B24317; $55972
                                                                                                      B30239
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Best Local Similarity
Tarches 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-453 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: F86846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: The complete genome sequence of the lactic A; Reference number: A86625; MUID:21235186; PMID:1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CC2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen; J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-422 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein CC2429 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: D87550
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;Experimental source: strain IL1403
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Best Local
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llarity 100.0%;
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                  revision 28-Feb-1990 #text_change 09-Jul-2004
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k; Pred. No. 11;
0; Mismatches
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0; Mismatches
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PMID:11337471
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                                      Matches
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A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Vanter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Deinococcus radjodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75451
                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9RVN1; GB:AE001951; GB:AE000513; NID:g6458712; PIDN:AAF1057:
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-75 < WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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F;331-347/Domain: transmembrane #status predicted <TM3>
F;402-418/Domain: transmembrane #status predicted <TM4>
F;502-518/Domain: transmembrane #status predicted <TM5>
F;681-697/Domain: transmembrane #status predicted <TM6>
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A;MOlecule type; DNA
A;Residues: 1-1045 <BAS>
A;Residues: 1-1045 <BAS>
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
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A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
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A;Cross-references: UNIPROT:P12684; EMBL:M22255; NID:g171687; PIDN:AAA34677.1;
A;Cross-references: UNIPROT:P12684; PIDN:AAA34677.1;
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A;Cross-refe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Basson, M.E.; Thorsness, M.; Rine, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 5563-5567, 1986
A;Title: Saccharomyces cerevisiae contains two functional A;Reference number: A94112; MUID:86287298; PMID:3526336
A;Accession: B24317
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C;Superfamily: hydroxymethylglutaryl-CoA reductase I
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A; Residues: 1-1045 < DUZ >
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A; Residues: 772-961 <BAS2>
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                                              Query Match
Best Local
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7; Conserv
    Similarity 6; Conserv
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t; Score 6; DB 2
t; Pred. No. 23;
0; Mismatches
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Pred. No. 23;
                                     DB 2;
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d <TM1>
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                                                                           Length 75;
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, L.; Utterback,
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T.; Zalewski,
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89932
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Fitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89932
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E89932
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82494
hypothetical protein BH1707 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: C83863
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82494
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A;Cross-references: UNIPROT:Q99TW8; GB:BA000018; PID:g13701324; PIDN:BAB42618.1; GSPDB:
A;Experimental source: strain N315
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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tive 0; Mismatcl
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Sekimizu,
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                                                                                                               hypothetical protein APE2197 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 C;Accession: H7527 C;Accession: H7527 R;Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyri A;Reference number: A72450; MUID:99310339; PMID:10382966
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertere C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choz A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

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A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A6580, MUID:98044033; PMID:9384377
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A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: C83863
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A;Molecule type: DNA
A;Residues: 1-131 <STO>
                                                                                                                                                                           A;Gene:
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A; Residues: 1-134 < KUN>
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus halodurans
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RESULT 13
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-146 <KAW>
A;Cross-references: UNIPROT:Q9Y9U2; DDBJ:AP000063; NID:g5105654; PIDN:BAA81208.1; PID:g5
A;Experimental source: strain K1
A;Experimental source: strain K1
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                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KOS>
                                                                                                                                                                                                  A;Reference number: S59503;
A;Accession: S59507
                                                                                                                                                                                                                    R;Koster, M.; Ovaa, W.; Bitter, W.; Weisbeek, Mol. Gen. Genet. 248, 735-743, 1995
A;Title: Multiple outer membrane receptors fo. A;Reference number: $59503; MUID:96069713; PM
                                                                                                                                                                                                                                                                                                             ferric pseudobactins receptor protein RF5 - Pseudomonas putida C;Species: Pseudomonas putida C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change
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R;Graham, S.W.; Barrett, S.C.H.
Submitted to the EMBL Data Library, November 1996
Submitted to the EMBL Data Library, November 1996
Submitted to the EMBL Data Library, November 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: H72527
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C;Species: chloroplast Galanthus nivalis (common snowdrop)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Reference number:
;Accession: T17044
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                                                                                                                                                                                                                                                                                               Accession: S59507
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                                                                       Similarity 6; Conserv
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100.0%; Pred. No. 50,
tive 0; Mismatches
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Search completed: February Job time: 15.5556 secs

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A;TITLE: Complete sequence and gene organization of the genome of a A;Reference number: A71000; MUID:98344137; PMID:9679194 A;Accession: C71193 A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.; Ohfuku, Y.; Funahashı, DNA Res. 5, 55-76, 1998 A;Title: Complete sequence
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Aug-2004
C;Accession: B75152
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C;Superfamily: Thermophilic adenylate cyclase, CyaB type
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A;Cross-references: UNIPROT:Q9V1Q2; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4929:
A;Experimental source: strain Orsay
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                                                                                                                                                                                                                                                                                                                                                               R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein PH1819 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: C71193
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Q9ASLB
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RA Sekime M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Salto K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwyanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwyanagi T., Wagatsuma M., Shiratori A.,
RA Minomiya K., Kamia K., Yokoi T., Puruya T., Kikkawa M., Yamazaki M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
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RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Antia M., Sato K., Arita M., Jano S.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
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RA Abaranaka R., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Alaushima-Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,
Chiba Y., Odara M., Hata H., Watanabe M., Komatsu T.,
Nakalima Y., Mizuno T., Mosuho Y., Yamashita R.,
Nakai K., Yada T., Nakamira Y., Ohara O., Isogai T., Sugano S.,
Taka Okumura K., Nakagima Y., Mizuno T., Ohara O., Isogai T., Sugano S.,
Taka Okumura K., Nakagima Y., Mizuno T., Shigata K.,
Nakagima M., Satoh T., Shigata K.,
Nakagima M., Satoh T.,
                                                                                                                  Q6P197 PRELIMINARY, PRT, 1106 AA. Q6P197; Q6P197; Q6P197; Q6P197; Q7-2004 (TrEMBLrel. 27, Created) O5-JUL-2004 (TrEMBLrel. 27, Last sequence update) O5-JUL-2004 (TrEMBLrel. 27, Last annotation update) PLJ10359 protein (Fragment).
   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                        Name=FLJ10359;
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Hypothetical protein FLJ40893.
Homo sapiens (Human)
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Fasher A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Fasher A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Fasher A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wolfin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

BOBAK S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley R.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butteerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.S., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Generation and initial analysis of more than 15,000 full-length human
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence up
02-MAR-2004 (TrEMBLrel. 27, Last annotation
FLJ10359 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008938;
NON TER 1
SEQUENCE 1106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLJ10359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH65205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH65205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R., submitted (JAN-2004) to the Submitted (JAN-2004) to the EMBL; BC065205; AAH65205.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISSUE=Lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909 LKGLFTLFAGHLVKPFADTLDQVNISKTDEAFFDSENDPEK 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Pred. No. 4.3e-3
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
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                                                                                                                                                                                                                                                                                                                                         CTISUE-Mammary tumor. WAP-TGF alpha model. 7 months old;
X MEDLINE-22388257; PubMed=12477932;
X MEDLINE-22388257; PubMed=12477932;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
X Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
X Altachenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Altachenko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Altachenko L., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,
X Altachenko M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
X Altachenko M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
X Altachenko M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,
X Altachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
X Altalan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Altalan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Altalan M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Altachenko M., Touchman J.W., Green E.D., Dickson M.C.,
X Altalan M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
X Altachenko M., Schmutz J., Myers R.M., Schein J.E.,
X Altachenko M., Schmutz J., Myers R.M., Schein J.E.,
X Altachenko M., Schmutz J., Myers R.M., Schein J.E.,
X Altachenko M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
X Altachenko M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Best I
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Q6VCK1;
01-MAR-2002
01-MAR-2002
                                                                                                                            SEQUENCE FROM N.A.
STRAIN=mix FVB/N;
TISSUE=Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                         Strausberg R.;
Submitted (DEC-2001) to the
EMBL; BC019693; AAH19693.1;
MGD; MGI:2384983; BC019693.
                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-mix FVB/N;
TISSUE-Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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Submitted (JAN-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                    "Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue-Lymph;
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-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
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                                                                                                                                                                                                                                                                                                                              .J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                                                                                                                                                                                                        on and initial analysis cDNA sequences.";
1. Acad. Sci. U.S.A. 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKGLFTLFAGHLVKPFADTLDQVNISKTDEAFFDSENDPEK
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2384983; BC019693.
IPR008938; ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequences.";
l. Acad. Sci. U.S.A.
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Rodentia;
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W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
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Best Local
                                     Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-len
enriched library, clone:6430400D06 product:hypothetical ARM
structure containing protein, full insert sequence.
                                                                                                                                                                                                                                           Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs t prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUE=Olfactory brain;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs,"; Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Olfactory
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=20530913; PubMed=11076861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Olfactory
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MEDLINE=99279253; PubMed=10349636;
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SEQUENCE
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Pred. No.
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H., Itoh M.,
, Harada A.,
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-I- SIMILARITY: Contains 1 HEAT repeat.
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osada N., Hida M., Kusuda J., Tanuma R., Iseki
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from maca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation updat
Protein BAP28 (QnpA-17571) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP28_MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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                                                                                                                                                                                                                                                                        AB049842; BAB16728.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:2384983; BC019693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                      Similarity
                                                                                                                                                                                          PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                            IPR008938; ARM. IPR000357; HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKGLFTLFAGHLVKPFADTL 230
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                                                                                                                    958 AA;
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                956
48.8%; 5cc
100.0%; Pr
                                                                                                                  108644 MW;
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(Fragment).
                                      Score 20;
Pred. No.
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                                                                                                                                                HEAT
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Pred. No.
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           Mismatches
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                                                                                                               3DBD95C3623CFB31 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from macaque brain
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J. 1.9e-12;
O;
                                 3.8e-12;
                                                             DB 1;
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                                                          Length 958;
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           Indels
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa E.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Takahashi Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Yamazaki M., Watanabe T., Satoh N., Takahashi Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Moniyama H., Satoh N., Takahashi S., Terashima Y., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takama S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mateumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Vanashita R.,
RT CDNAs.",
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Q9H583; Q9NW23;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
05-JUL-2004 (Rel. 4
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14702039; DOI=10.1038/ng1285; Ota T., Suzuki Y., Nishikawa T., Ote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
Cobley V.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A novel BAP28 gene and protein
Patent number WO0100669, 04-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel BAP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bougueleret L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein BAP28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                . Genet. 36:40-45(2004).
SIMILARITY: Belongs to the BAP28 far
SIMILARITY: Contains 1 HEAT repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chumakov I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40, Created)
40, Last sequence 44, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Chordata;
; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      780
                                                                                                                                                                                                         BAP28 family.
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R EMBL; AJ431206; CAD24024.1; -.

R GO; GO:0009507; C:chloroplast; IEA.

R GO; GO:0009507; C:chloroplast; IEA.

R GO; GO:0009523; C:photosystem II; IEA.

R GO; GO:00016431; F:oxidoredystem II; IEA.

R GO; GO:0016431; F:oxidoreductase activity; IEA.

R GO; GO:0016431; F:oxidoreductase activity; IEA.

R GO; GO:001642773; P:ATP synthesis coupled electron transport; IEA.

R GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.

R InterPro; IPR003945; NADHUD_oxred5.

R InterPro; IPR001750; Oxidored q1.

R InterPro; IPR001750; Oxidored q1.

R InterPro; IPR001516; Oxidored q1.

R InterPro; IPR001516; Oxidored q1.

R Pfam; PF00361; Oxidored q1.

R Pfam; PF001010; Oxidored q1.

R Pfam; PF001010; Oxidored q1.

R Pfam; PF001010; Oxidored q1.

R Pfam; PF001014; NADHUDGNASE5.

R TIGERNA; FR01434; NADHUDGNASE5.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism.
REPEAT 2106
VARIANT 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bremer B., Bremer K., Heidari N., Erixon P., Olmstead R.G., Anderberg A.A., Kallersjo M., Barkhordarian E.; "Phylogenetics of asterids based on 3 coding and 3 non-coding chloroplast DNA markers and the utility of non-coding DNA at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Solanales; Montiniaceae; Kaliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8M9G5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL136105; CAC159
EMBL; AK001221; BAA915
SWISS-2DPAGE; Q9H583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           taxonomic levels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=125030;
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                         TIGR01974;
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BAA91564.1; ALT_INIT.
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SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus J.

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus J.

Kapatral V., Bhattacharyya A., Larsen N., D'Souza M., Walunas T.,

Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Chu L., Mazur M., Goltsman E., Larsen N., Fonstein M., Ehrlich S.D.,
                                                                                             SEQUENCE FI
                                                                                                                                                                                                                                                           Q87Z92 PRELIMINARY; PRT; 273 AA. Q87Z92; Q1-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Bacterial transferase, havapeptide repeat protein orderedLocusNames=PSPTO3538;
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MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100; Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T. Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.
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EMBL; AE017005; AAF09293.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0046873; F:metal ion transporter

GO; GO:0030001; P:metal ion transport; I
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                                                                                                                                                                                                             Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pfam; PF02535; Zip; 1.
SEQUENCE 245 AA; 27087 MW; EF5C8D3CEF89C934 CRC64;
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01-JUN-2003
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Bacillaceae;
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Q9AAU6;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                            InterPro; IPR003169; GYF.
InterPro; IPR010432; RDD.
Pfam; PF06271; RDD; 1.
Complete proteome; Hypothetical
SEQUENCE 296 AA; 32415 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=ATCC 19089 / CB15;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Bermoleva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein CC0498.
OrderedLocusNames=CC0498;
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE005722; AAK22485.1; PIR; A87311; A87311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
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Khouri H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of Caulobacter crescentus.", roc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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100.0%; Pred. No. 59;
tive 0; Mismatches
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100.0%; Pred. N
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B9D92D2D8A921156 CRC64;
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RESULT 13

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Q8HS77;
01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002
01-JUN-2002
01-OCT-2003
                           MEDLINE-22431356; PubMed=12542710;
Matsuo Y., Suzuki M., Kasai H., Shizuri Y., Harayama S.;
"Isolation and phylogenetic characterization of bacteria capable of inducing differentiation in the green alga Monostroma oxyspermum.";
Environ. Microbiol. 5:25-35 (2003).
-i- FUNCTION: DNA gyrase negatively supercoils closed circular doublestranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded interconversion of other topological isomers of double-stranded
                                                                                                                                                                                                                                                                                                                          Bacteria; Bacteroidetes; Sphin
Cremotrichaceae; Chitinophaga.
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=79329;
                                                                                                                                                                                                                                                                                                                                                                         Chitinophaga pinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA gyrase subunit B
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GO; GO:0009523; C:photosystem II; IEA.
GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Whitlock B.A., Karol K.G., Alverson W.S.;
Chloroplast DNA sequences confirm the placement of the
Ceanopapaver within Corchorus (Grewioideae: Malvaceae s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Malvales; Malvaceae; Grewioideae; Corchorus.
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Chloroplast.
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DNA rings, including CATALYTIC ACTIVITY:
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7; Conserve
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366 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
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                   including catenanes and knotted rings (By similarity)
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C -!- SIMILARITY: Belongs to the type II topoisomerase family.

EMBL; AB073077; BAB88379.1; -.

REMBL; AB073077; BAB88379.1; -.

REMBL; AB073077; BAB88379.1; -.

REMBC; P06982; IAJ6.

REMBC; P06982; IAJ6.

REMBC; P06982; F:ATP binding; IEA.

GO; GO:0003524; F:ATP binding; IEA.

GO; GO:0003524; F:NA binding; IEA.

GO; GO:000318; F:NA topoisomerase (ATP-hydrolyzing) activity; IEA.

REMBC; P06982; F:NA topoisomerase (ATP-hydrolyzing) activity; IEA.

REMBC; P06982; F:NA topoisomerase.

REMBC; GO:0016853; F:isomerase activity; IEA.

REMBC; GO:0016853; F:isomerase activity; IEA.

REMBC; GO:0016853; F:isomerase (ATP-hydrolyzing) activity; IEA.

REMBC; GO:0003216; F:NA topoisomerase.

REMBC; GO:0003216; F:NA topoisomerase.

REMBC; GO:0003216; F:NA topoisomerase.

REMBC; GO:0003216; F:NA topoisomerase.

REMBC; GO:0003216; F:NA topoisomerase.

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REMBC; GO:00032
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STRAIN-RIMD 2210633 / Serotype 03:K6;

MEDLINE-2508454; PubMed-12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

EMBL; AP005078; BAC5908.1; -.

InterPro; IPR007400; DUF453.

Fiam; PP04303; DUF453; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=VP1645;
Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein VP1645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Hypothetical protein. SEQUENCE 398 AA; 42358 MW; 8CFE4C76CED989B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=670;
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100.0%; Pred. No. 75;
Live 0; Mismatches
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OM protein - protein search, using sw model
                                                                         Copyright
                                                                     GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Run on: February 1, 2005, 15:09:39; Search time 59.7778 Seconds (without alignments) 247.799 Million cell updates/sec

Scoring table: Title: Sequence: Perfect score: Gapop 60.0 , Gapext 60.0 OFIGO SEQSGLU2017 NCLYKIFLFDTQHFISKERA.....ALMMPLVDQLENRLGGEEKF

41

Searched: 1608061 ведв, 361289386 residues

Word size :

0

Total number of hits satisfying chosen parameters:

Minimum Maximum DB 80 seq length: 21
seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:\*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:\*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:\*

4: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:\*

6: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:\*

6: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:\*

7: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6677777777	Score
100.0 19.5 17.1 17.1 17.1 17.1 17.1 17.1 17.1 17	Query Match
1149 378 378 348 349 660 660 456	Query Match Length DB
155 155 155 156 156 156 157	DB
US-10-128-558-167 US-10-282-122A-49544 US-10-424-59-275868 US-10-767-701-4175 US-10-369-493-22801 US-10-424-599-149524 US-10-427-114-55502 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-151847 US-10-437-963-14933 US-10-424-599-149522 US-10-424-599-149522 US-10-425-115-340619	ID
Sequence 167, App Sequence 49544, A Sequence 275868, Sequence 21775, A Sequence 12801, A Sequence 149524, Sequence 110319, Sequence 110349, Sequence 151847, Sequence 110342, Sequence 149522, Sequence 149522, Sequence 149522, Sequence 149523, Sequence 149532, Sequence 340619,	Description

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-10-437-963-	-10-117	-10-117-087-4	US-10-425-114-41418	-10-4	0-424-599-2	-10-425-114-3	-10-425-115-2	-10-437-963-1	-10-425-115-2	-10-425-115	-10-424-	-10-767-701	-10-627-476-9	-10-282-122A	-10-437-963-	-10-437-963	-10-767-701	-10-425-115	-10-425-115-	-10-425-115	-10-	-10-389-647	-28	-127-032	US-09-815-242-12049	-10-424-599-2	-10-425-115-2	-10-029-386-	US-10-424-599-219715	US-10-425-115-339911	US-09-989-920-197
e 102617,	6. Appl		e 41'	Ф	e 2	Sequence 39348, A	Ø	æ	ø			546	e 94, A	e 52746,	13798		e 54325	æ	Œ	266	17893	Sequence 644, App	66719	e 135,	Sequence 12049, A	24564	Ø	M	219	e 3399	Sequence 197, App

## ALIGNMENTS

RESULT 1
US-10-128-558-167
; Sequence 167, App.; Publication No. 1 PRIOR APPLICATION NUMBER: US 60/339,453
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR PPLICATION NUMBER: PCT/US00/35017
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2001-01-25
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PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2000-02-28
PRIOR PILING DATE: 2000-02-28 GENERAL INFORMATION: FILE REFERENCE: 812A
CURRENT APPLICATION NUMBER: US/10/128,558
CURRENT FILING DATE: 2002-04-22 APPLICANT: Boyle, Bryan J
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides APPLICANT: Tang, Y. Tom APPLICANT: Wang, Zhiwe Prior Application data removed - See File Wrapper or PALM. Wang, Zhiwei Weng, Gezhi Boyle, Bryan J Application US/10128558 US20040219521A1

; SOFTWARE: pt\_FL\_genes Ver ; SEQ ID NO 167-; LENGTH: 1149 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-128-558-167

NUMBER OF SEQ ID NOS:

\_FL\_genes Version

6.0

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1002 NCLYKIFLFDTQHFISKERAEALMMPLVDQLENRLGGEEKF 1042

1 NCLYKIFLFDTQHFISKERAEALMMPLVDQLENRLGGEEKF 41

Matches

41; Conservative

Query Match Best Local Similarity

100.0%; Score 41; DB 17; Length 1149; 100.0%; Pred. No. 1.8e-33;

Mismatches

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Indels

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Gaps

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US-10-282-122A-49544

Sequence 49544, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:

Zamudio, Caric Malone, Cheryl

Liangeu

Haselbeck, Robert

Ohlsen, Kari Zyskind, Judith

Daniel

t, John

APPLICANT: APPLICANT: RESULT 2

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                                                                                                                     Matches
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LENGTH: 378
                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                   ORGANISM: Burkholderia fungorum
                                                                                                                   Local Similarity
les 8; Conserv
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
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FILING DATE: 2000-12-22
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FILING DATE: 2000-11-27
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FILING DATE: 2000-10-23
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                                                                                                                     Conservative
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                                                                                                                 19.5%; Score 8; 1
100.0%; Pred. No.
Live 0; Mismatcl
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                                                                                                                   Mismatches
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RESULT 5
US-10-369-493-22801
Sequence 22801, Application US/10369493
Publication No. US20030233675A1
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C6863_1.pep US-10-767-701-41775
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US-10-424-599-275868
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GENERAL INFORMATION:
APPLICANT: Cao, Yon
APPLICANT: Hinkle,
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(55535)B

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 41775

LENGTH: 238

TYPE: PRT

ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                           Matches
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SEQ ID NO 275868
LENGTH: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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Cao, Yongwei
Hinkle, Gregory J
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100.0%; Pred. No.
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Pred. No.
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o. 11;
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US-10-425-114-53502

/ Sequence 53502, Application US/10425114

/ Publication No. US20040034888A1
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; TYPE: PRT
; ORGANIZM: Schizosaccharomyces pombe
US-10-369-493-22801
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                                                                                                                             GENERAL INFORMATION:
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SEQ ID NO 149524
LENGTH: 349
TYPE: PRT
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SEQ ID NO 22801
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                                                     APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_106042C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(349)
OTHER INFORMATION: unsure at all Xaa locations
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Zhou, Yinua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                  Similarity
7; Conserv
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100.0%; Pred. No.
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o. 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 110339
LENGTH: 633
TYPE: PRT
                                                                                                                                                                           GENERAL INFORMATION:
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Best Local
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                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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PPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_14411C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Oryza sativa
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nes 7; Conserv
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                                                    Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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Wu, Wei
                                        Barbazuk, Brad
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100.0%; Pred. No.
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100.0%; Pred. No.
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Best Local Similarity
Warches 7; Conserve
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US-10-437-963-151847
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Best Local Similarity
Matches 7; Conserv
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SEQ ID NO 110342
LENGTH: 662
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                                                                                                           APPLICANT:
       APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules.
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 151847
LENGTH: 660
                                                                                                                                            APPLICANT: La Rosa Thomas J
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
FEATURE:
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                     588 PLVDQLE 594
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SEQ ID NOS: 285684
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                                                                                                                           Zhou Yihua
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Barbazuk, Brad
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o. le+02;
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Patent No. US20020048763A1
GENERAL INFORMATION:
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LENGTH: 665
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                            TUMBER OF
                                       RIOR APPLICATION NUMBER: US 09/774,203
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR FILING DATE: 2000-09-27
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ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(665)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                            APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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Annomax Sequence Listing Engine vers. 1.1
                          SEQ ID NOS: 49117
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Pred. No.
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SEQ ID NO 340619
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LENGTH: 36
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Best Local :
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                                                                         APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
CURRENT FILING DATE: 2001-11-21
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TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2003-04-28
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGN OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0
OTHER INFORMATION: EXPRESSED IN BLONE MARROW, SIGNAL = OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGN OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GGEEKF 9
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6; Conserv
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IN BRAIN, SIGNAL = 0.86
IN LUNG, SIGNAL = 1
IN BONE MARROW, SIGNAL = 1.1
IN ADULT LIVER, SIGNAL = 0.86
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; SEQ ID NO 197
; LENCTH: 48
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-920-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-425-115-339911
; Sequence 339911, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Best Local Similarity
Grethes 6; Conserve
Search completed: February 1, 2005, 15:44:52 Job time : 59.7778 secs
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                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_73167C.1.pep US-10-425-115-339911
                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 339911
                                                                                                                                  Query Match
Best Local
                                                                                                                     Matches
                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(49)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                             ENGTH: 49
                                                          21 RAEALM 26
                                                                                     19 RAEALM 24
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 21 seq length: 2000000000
   Query
Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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                                                                                                       140369
D39384
E70385
AE1538
T21208
G650309
F90919
C85768
D64918
D64918
E83379
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H69173
B41845
AE0883
RRNZ18
E90239
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291.016 Million cell updates/sec
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22K factor - human
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                                                                                                                                                                                                                                                                                          ribosomal RNA
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Query Match Best Local Similarity Thes 7; Conserve

Conservative

0

100.0%; 17.1%;

Score 7; DB 2; Pred. No. 7.4; O; Mismatches

Length 276; Indels

0

Gaps

0

RESULT 2 AG3305 ZS ribosomal R C;Species: Bruc C;Date: 01-Feb- C;Accession: AG C;Accession: AG C;Accession: AG AZUC, M.; Mazur, M.; G Proc. Natl. Aca A;Title: The ge A;Accession: AG A;Ccession: AG A;Status: preli A;Molecule type A;Residues: 1-2 A;Cross-referen A;Cross-referen A;Experimental C;Genetics: A;Gene: BMEI042 A;Mag position: C;Keywords: met	RESULT 1 JC7708 beta crysta C;Species: C;Species: C;Acate: 09- C;Accten, J: Biochem. B: A;Title: Mc A;Reference A;Acotesiou A;Molecule A;Residues A;Croment: C;Superfam. C;Superfam. F;20-25/Res Query Mat Best Loca Matches Qy Db	
NA methyltransferase (EC 2.1.1) [imported] - Bru ella melitensis 2002 #sequence_revision 01-Feb-2002 #text_change 0 3305 .G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, oltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; d. Sci. U.S.A. 99, 443-448, 2002 d. Sci. U.S.A. 99, 443-448, 2002 ser: AD3252; PMID:11756688 3305 minary . DNA 76 .KUR> 76 .CKUR> 76 .CKUR> 76 .CKUR> 76 .CKUR> 76 .CKUR> 77 .CCES: UNIPROT:Q8YIL5; UNIPROT:Q8FZA1; GB:AE008917; 80urce: strain 16M 9 I I	allin Bl protein - zebra fish  Bracchydanio rerio (zebra fish)  Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09- n: JC7706  X: Chang, B.E.; Chen, Y.H.; Lin, C.J.F.; Wu, J.L.; Kuo, iophys. Res. Commun. 285, 105-110, 2001  Notecular cloning, developmental expression, and hormonal enumber: JC7706; MUID:21331298; PMID:11437379  n: JC7706  Tris protein is involved in regulation by growth factors ferences: UNIPROT:090WT1; GB:AJ317957  Ferences: UNIPROT:090WT1; GB:AJ317957  ill; beta-crystallin  ggion: active proline- and alanine-rich motif #status pred atch  17.1%; Score 7; DB 2; Length 232;  al Similarity 100.0%; Pred. No. 6.3;  7; Conservative 0; Mismatches 0; Indels 0;  4 YKIFLFD 10	6 14.6 251 2 C84036 6 14.6 251 2 C83083 6 14.6 251 2 C83083 6 14.6 262 2 C83265 6 14.6 264 2 G83165 6 14.6 268 2 T02448 6 14.6 269 2 AD2833 6 14.6 270 2 D99542 6 14.6 281 2 T43945 6 14.6 283 2 H97610 6 14.6 283 2 H97610 6 14.6 292 2 B41656 6 14.6 295 2 D90252 6 14.6 302 2 T08522 6 14.6 302 2 S72151 6 14.6 302 2 S72151 6 14.6 302 2 S72151 6 14.6 302 2 C87293  ALIGNMENTS
cella melitensis (strain 9-Jul-2004   C.; Los, T.; Ivanova, lo'Callaghan, D.; Letesson hogen Brucella melitens:	09-Jul-2004 10, C.M. 1al regulation of zebraficers. 20078. 20078. 30; Gaps 0;	nate dehydrog rrved hypothet hetical prote ble ATP-bindi hetical prote 'family prote rrved hypothet comal protein hetical prote chain alcoho lamycin resist rrved hypothet inding protei jinding protei protein homol hetical prote

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R;Shearman, C.A.; Godon, J.J.; Gasson, M.
Mol. Microbiol. 21, 45-53, 1996
A;Title: Splicing of a group II intron in a functional if A;Reference number: S77646; MUID:97000348; PMID:8843433
A;Accession: S77647
A; Molecule type: DNA
                                                                                                          C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 C;Accession: S77647
                                                                                                                                         mobilisation protein A - Lactococcus lactis self-transfer sex factor C_\ell Species: Lactococcus lactis
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A;Residues: 1-396 <HAR>
A;Cross-references: UNIPROT:Q38033; EMBL:X76288; NID:g432610; PIDN:CAA53908.1; PID:g5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hartley, N.M.; Murpl submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 12 - phage phi-C31
C;Species: phage phi-C31
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: S38924
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A; Accession: S38924
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A;Residues: 1-362 <SEE>
A;Cross-references: UNIPROT:074975; EMBL:AL023777; PIDN:CAA19310.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-, cosmid c1827
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A;Reference number: 221974
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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0; Mismatches
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o. 9.3;
                                                 functional transfer
                                                                                                                       #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                   Length 396;
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R;Damme, J.V.; De Ley, M.; Opdenakker, G.; Billiau, A.; De Somer, Nature 314, 266-268, 1985
A;Title: Homogeneous interferon-inducing 22K factor is related to A;Reference number: A21851; MUID:85163727; PMID:3920526
A;Accession: A21851
A;Cross-references: UNIPROT:Q7M4S7C;Superfamily: interleukin-1
                                     A; Molecule type: protein A; Residues: 1-38 < DAM>
                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 09-Jul-2004
C;Accession: A21851
                                                                                                                                                                                                                                                                                                 RESULT 7
A21851
                                                                                A; Status: preliminary
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F;121-187/Domain: ribonucleoprotein repeat homology <RRM2:
F;212-278/Domain: ribonucleoprotein repeat homology <RRM3:
F;315-381/Domain: ribonucleoprotein repeat homology <RRM4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: polyadenylate-binding protein; ribonucleoprotein C;Keywords: nucleus; RNA binding F;33-100/Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P93616; EMBL:U81318; NID:g1737491; A;Experimental source: sprout tips from 5 day old growing sprou C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The wheat poly(A)-binding protein functionally A;Reference number: Z12044; MUID:97182620; PMID:9030759 A;Accession: T06979
                                                                                                                                                                                                                                                                             22K factor -
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A; Residues: 1-651 <LEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyadenylate-binding protein - wheat
N;Alternate names: poly(A)-binding protein
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
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A;RCross-references: EMBL:X89922; NID:g1296826; PIDN:CAA61995.1; PID:g1296828
A;Experimental source: strain MG1363
C;Genetics:
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0; Mismatches
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15;
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A; Gross-references: UNIDROT: P37812; EMBL: Z28592; NID: 9433983; PIDN: CAA82261.1; PID: 94339 A; Gross-references: UNIDROT: P37812; EMBL: Z28592; NID: 9433983; PIDN: CAA82261.1; PID: 94339 A; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallzzi, A.; Galleriech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Saro, T.; Scanlon, A; Authors: Schleich, S.; Schroeteer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serorakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchyama, A; Minters, P.; Migat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; The complete genome sequence of the Gram-postive bacterium Bacillus subtilis. A; Reference number: A69580; MUID: 98044033; PMID: 9384377
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-132 <RES>
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Nature 406, 959-964, 2000
  A;Accession: G69591
A;Status: nucleic a
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A; Residues: 1-65 <STO>
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A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E70385
                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein aq_987 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Accession: E70385
                                                                                                                                                                                                                                                                                                                                                                                     RESULT
E70385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-154 <BEL>
A;Cross-references: GB:M61869; NID:g184449; PID:g184450
C;Superfamily: zinc finger protein ZPP-36; LIM metal-binding
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: D39384
R;Bellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991
A;Title: The evolutionarily conserved Krueppel-associated A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Accession: D39384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15697.1; PID:g2636205
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                          A;Residues: 1-165 <AQF>
A;Cross-references: UNIPROT:O67112;
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change
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39384
finger protein HTF6 - human (fragment)
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                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not
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A;Molecule type: DNA
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Matches
                                                                                          ;Gene: aq 987
;Superfamily:
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Best L
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                                           Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                        G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
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RLGGEE 39
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                                                                                          abyssi hypothetical protein PAB0445
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Pred. No.
                                               Pred.
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                                     DB .
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C;Date.
C;Accession: G650.
R;Blattner, F.R.; Plunkett 111,
R.; Rose, D.J.; Mau, B.; Shao
A.; Rose, 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                               hypothetical protein b2612 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G65039
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A;Reference number: Z19390
A;Accession: T21208
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21208
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A; Residues: 1-188 <WIL>
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; M. ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ent D.; Jones, L.M.; Karst, U.
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A;Residues: 1-184 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: CESP:F21D9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source:
                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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Best Local (
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Experimental source: strain Clip11262
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lau, B.; Shao, Y.
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100.0%; Pr
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s; Pred. No. 61;
0; Mismatches
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                                                                             Bloch,
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tian, K.D.;
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; Fsihi, H.
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                                                                                                                C;Genetics:
A;Gene: ECs2326
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                  A;Cross-references: UNIPROT:Q59431; GB:BA000007; A;Experimental source: strain O157:H7, substrain
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-196 < HAY>
                                                                                                                                                                                                                              A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                repressor for uid operon [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0: C;Species: Escherichia coli C;Decies: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: F90919
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                                          Best Loc
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N.; Yasunaga, T.; Kuhara, S.;
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HFISKE 18
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                                    14.6%; Score 6; DB larity 100.0%; Pred. No. 63 Conservative 0; Mismatches
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Pred. No.
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Shiba, T.;
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63;
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; Hattori, M.; Shinagawa,
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C.G.

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Maximum DB seq length: 2000000000
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1: uniprot_sprot:*
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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RY SEQUENCE OF 1777-2144 FROM N.A.

RY PubMed=14702039, DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makite H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai T., Isayanagi T., Wagateuma M.,

RA Yamamoto J.-I., Saito K., Kawai T., Iwayanagi T., Wagateuma M.,

RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagateuma M.,

RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagateuma M.,

RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagateuma M.,

RA Nagawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

RA Omura Y., Abe K., Kamihara K., Katsuta N., Saco K., Tanikawa M.,

RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

RA Ishida S., Ono Y., Takiguchi S., Watenabe M., Hiraoka S., Chiba Y.,

RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki M., Aotsuka S.,

RA Nomura Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Yamazaki M., Watanabe K., Kumada T., Takemoto M., Kawakami B.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagi A., Tiakura S., Fukuzumi Y.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Matsumura K., Nakajima Y., Mizuno T., Kohanabi Y., Nakagawa K.,

RA Mizushima Sugano J., Satoh T., Shirati Y., Takahashi Y., Nakagawa K.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Complete sequencing and characterization of 21,243 full-length human
EMBL; AX067150; CAC26776.1; -.
EMBL; AL136105; CAC15948.1; -.
EMBL; AK001221; BAA91564.1; ALT_INIT.
SWISS-2DPAGE; O9H583; HUMAN.
InterPro; IPR008938; ARM.
InterPro; IPR008357; HEAT_REPEAT; FALSE_NEG.
POLYMOZPhism.
REPEAT 2106 2142 HEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Genet. 36:40-45(2004).
-!- SIMILARITY: Belongs to the BAP28 family.
-!- SIMILARITY: Contains 1 HEAT repeat.
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16-OCT-2001
05-JUL-2004
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Mammalia; Eutheria; Primates;
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0;	Matches 22; Conservative 0; Mismatches	8
	Similarity 100.0%; Pred. No. 1.1e-14;	
	SUDMITTED (DEC-2001) to the EMBL/GenBank/DDBJ databases.  EMBL; BC019693; AAH19693.1;  MGD; MGI:2384983; BC019693.  InterPro; IPR008938; ARM.  SEQUENCE 349 AA; 40166 MW; 9763D0331AD0F515 CRC64;	SCRUCK
	SEQUENCE FROM N.A.  STRAIN=mix FYDEN; TISSUE=Whammary tumor. WAP-TGF alpha model. 7 mont Strausberg R.;	2 2 2 2 2 2 3 2 2 2 2
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	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J. Jones S.J., Marra M.A., "Genevation and initial collection of distinct and collection of december."	2222
	<pre>xichards S., Worley K.C., Hale S., Garcia A.M., Gay Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gi Fahey J., Helton E., Ketteman M., Madan A., Rodrigue Whiting M., Madan A., Young A.C., Shevchenko Y., Boulden B. Blakesley R.W., Touchman J.W., Green R. D. Dicken M. Blakesley R.W., Touchman J.W., Green R. D. Dicken M.</pre>	22222
	Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.	2222
	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
	SEQUENCE FROM N.A.  STRAIN=mix FVB/N;  TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months ol  MEDLINE=22388557; PubMed=12477932;  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.C	전 전 전 전 전 전
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	F 41	D
0,	Query Match 100.0%; Score 41; DB 1; Length 2144; Best Local Similarity 100.0%; Pred. No. 4.5e-34; Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps	
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QBCCT5,
01-MAR-2003
                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUE-Olfactory brain;

MEDLINE-20530913; PubMed-11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Itogami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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STRAIN-C57BL/6J; TISSUE-Olfactory brain;

STRAIN-C57BL/6J; TISSUE-Olfactory brain;

MEDLINE-20499374; PubMed-11042159;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayyashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs

prepare full-length cDNA libbaries for rapid discovery of new

Genome Res. 10:1617-1630(2000).
                         STRAIN-C57BL/6J; TISSUE-Olfactory brain; Adachi J., Aizawa K., Akimura T., Arakawa T., Bono Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizu Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kurihara C., Matsuyama T., Miyazaki A., Murata M.,
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430400D06 product:hypothetical ARM repo
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; T
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Mammalia, Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-Olfactory brain.
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Nature 409:685-690(2001).
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Sciurognathi; Muridae; Murinae; Mus
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f., Bono H., ..
, Hashizume W.,
raoka T., Hirozane T.,
I., Kasukawa T.,
Youda M., Koya S
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Phey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                  Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC011983; AAH11983.1; -.
InterPro; IPR008938; ARM.
SEQUENCE 349 AA; 39921 MW; 3A359597FF7079EB CRC64;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                           rissum=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.;
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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J., Salto K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Yamamoto J., Salto K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa E., Omura Y.,

RA Abe K., Kamihara M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Amasahi M., Kiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Actsuka S.,

Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Noriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,

RA Pujinori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Ono T., Yamada K., Pujii Y., Ozaki K., Hirao M., Omori Y.,

RA Ono T., Yamada K., Mizuno T., Morinaga M., Sasaki M.,

RA Mizushima S., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,

RA Mizushima Sugano J., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,

RA Mizushima S., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,

RA Mizushima S., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,

RA Mizushima S., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,

RA Mizushima S., Satoh T., Shizai Y., Takahashi Y., Nakagawa K.,

RA Mizushima S., Satoh T., Shizai Y., Sasaki M.,

RA Mizushima S., Satoh T., Shizai Y., Sasaki M.,

RA Mizushima S., Satoh T., Shizai Y., Sasaki M.,

RA Mizushima S., Satoh T., Shizai Y., 
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                                                          Q6P197;
Q6P197;
05-JUL-2004
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FLJ10359 prot
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Q8N7L7;
01-OCT-2002
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                                FLJ10359 protein (Fragment)
Name=FLJ10359;
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Ota T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=Uterus;
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Homo sapiens (Human).
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                                                                             (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                               PRELIMINARY;
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   (Human)
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Boaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                           TISSUE=Lymph;
MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           PubMed=12477932;
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Primates;
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Grouse L.H., Derge J.G.,
vaner L., Shenmen C.M., Schuler G.I.
Schaefer C.F., Bhat N.K.
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Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Peldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
"The genome sequence of the anaerobic, suffate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
Nat. Biotechnol. 22:554-559(2004).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ABC transporter, ATP-binding protein.
OrderedLocusNames=DVU1627;
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SEQUENCE
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases EMBL; BC065205; AAH65205.1; -.
                                                                                                                                                                                                                                                                                                                                              EMBL; AE017314; AAS96105.1; -.
TIGR; DVU1627; -.
GO; GO:0005524; F:ATP binding; IEA.
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05-JUL-2004
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                                                                                                      ATP-binding; Complete proteome.
SEQUENCE 241 AA; 26639 MW;
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                                                                                                                                                                                                                    SMART; SM00382; AAA;
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA ATPase
InterPro; IPR003439; ABC_transporter
Pfam; PF00005; ABC_tran; 1.
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AAS96105;
27-APR-2004
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                                                                 Garner F.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ
EMBL; AL732629; CAE17602.1; -.
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cyprinidae; Danio.
                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SI:zC146F4.2.2 (Novel protein similar to human BAP2
                                                                                                                                                                                                                                                                      Q7T153
                                                            EMBL; AL732629;
                                                                                                                                                                                  Name=SI:zCl46F4.2;
Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding.
SEQUENCE 241 AA;
                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Biotechnol. 22:554-559
EMBL; AE017314; AAS96105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PubMed=15077118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desulfovibrionaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVU1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC transporter, ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-2004
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVU1627; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                   KERAEALM 122
                                                                                                                                                                                                                                                                                                                                                        KERAEALM 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KERAEALM
                                                 1278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TremBLrel. 27, Created)
(TremBLrel. 27, Last sequence update)
(TremBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                              Conservative (
  Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  26639
             19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrio.
                                                 143523 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                Score 8; DB 2
;; Pred. No. 4.5
0; Mismatches
  ..
             Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                   (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                  B9A37B368194F6FD CRC64;
  Mismatches
                                                 E6C9FC81B77EE1A9 CRC64;
            No.
                                                                                                                                                                                                                                                                       1278
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       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                           Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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                         Length 1278;
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  Indels
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PLVDQLEN 33

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PLVDQLEN 1221

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RESULT 12
Q7T152
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                                                                   RX MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B stownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Weckernan K.J., Malek J.A., Gunaratte P.H.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Winting M., Tuchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Browninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.;
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Best Local S
Matches 8
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Q7SY48;
01-OCT-2003
01-OCT-2003
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Name=SI:ZC146F4.2;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Actinopterygii; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7T152
Q7T152;
01-OCT-2003
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TremBLrel. 25, Last annotation update)
                                    "Generation and initial analysis of more
                                                         Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases EMBL, AL732629; CAE17603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                      mouse
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8; Conserv
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                      CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio.
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llarity 100.0%; Pred. No. 17
Conservative 0; Mismatches
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                  sequences.";
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    S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
    99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA949557F21ACBCE
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5. 17;
                                       than 15,000
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                                    full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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27

Query Match Best Local S Matches 7

Similarity 7; Conser

17.1%; Score 7; DB 100.0%; Pred. No. 21 :ive 0; Mismatches

DB 1;

0

Indels

0

Gaps

0

Length 80;

Nuclease. F6A CRC64;

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EX7S
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Best Local S
Matches 8
or senu ....

EMBL; APOS075; BAC58951.1; -.

HAMAP; MF_00337; -; 1.

InterPro; IPR003761; Exonuc_VII_S.

Pfam; PF02609; Exonuc_VII_S.

Pfam; PF02609; Exonuclease; Hydrolase; Nuc.

OR79 MW; 03B881D68BEC4F6A
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5' to 3'-or 3'- to 5'-direction to yield nucleoside 5'.phosphates.
-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RIMD 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EX7S VIBPA STANDARD; PRT; 80 AA 087RT8; 10-0CT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ
EMBL; BC055128; AAH55128.1; -.
Hypothetical protein.
SEQUENCE 2159 AA; 242048 MW; F00DBBA1D597E
                                                                                                                                                                                                                                                                                                                                                                                                              distinct from that of V. cholerae."; Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales, Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable exodeoxyribonuclease VII small subunit (EC (Exonuclease VII small subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIBPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=xseB; OrderedLocusNames=VP0688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AB;
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                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the xseB family.
                                                                                                                                                                                                                                                                                                 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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LVDQLEN 27

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RESULT 15
EX75 VIBVU
ID EX75 VIBVU
AC QBDFA5;
DT 10-CCT-2003
DT 10-CCT-2003
DT 10-CCT-2003
DT 10-CCT-2003
DT 05-ULL-2004
DE PROBABLE exc
EXCOUNCE PRO
GO VIBTIONACEAR
OX NCBI_TAXID=0
RP SEQUENCE PRO
RC STRAIN=CMCP,
RA Choy H.E.;
RT "Complete 9
RL SUBUNIT
CC -1- FUNCTIO
CC -1- CATALYT
CC -1- SUBUNIT
CC -1- SUBUNIT
CC -1- SUBULIAR
CC -1- SUBULIAR
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Search completed: February
Job time : 71.5556 secs
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
(Exonuclease VII small subunit).
Name-xseB; OrderedLocusNames=VV10313;
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HAMAP; MF_00337; -; 1.

InterPro; IPR003761; Exonuc_VII_S.

Pfam; PF02609; Exonuc_VII_S; 1.

TIGRPAMB; TIGR01280; xseB; 1.

Complete proteome; Exonuclease; Hydrolase; Nuclease.
SEQUENCE 80 AA; 8756 MW; FE23B015BD49F5ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=CMCP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong Choy \text{H.E.};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=672;
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Maximum DB seg length: 200000000
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/laa/backfiles1.pep:*
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US-09-347-833-4
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US-09-621-976-451
US-09-248-796A-22566
US-09-248-796A-22566
US-09-526-542-4
US-09-526-542-6
US-09-526-542-6
US-10-117-087-6
PCT-US95-05741-11
US-08-482-142-193
US-08-482-142-193
US-08-488-296-193
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US-08-1882-704A-2
US-09-151-957-2
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6451, Ap
22566, A
5651, Ap
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US-09-252-991A-26709 US-09-248-796A-2469 US-09-248-796A-2489 US-09-489-039A-11474 US-09-270-767-8539 US-09-270-767-43443 US-09-270-767-43443 US-09-270-767-43443 US-09-252-991A-25195 US-09-543-681A-7983 US-09-543-681A-7983 US-09-543-681A-7983 US-09-26A-11 US-09-252-991A-17027 US-09-252-991A-1391 US-09-252-991A-1391 US-09-387-418A-13 US-09-387-418A-13 US-09-387-418A-13 US-09-387-418A-13 US-09-387-418A-13	4	w	4	4	w	4	4	N	N	4	4	4	4	4	4	4	4	•
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	19301, A	10, Appl	14027, A	25307, A	13, Appl	14941, A	17027, A	12, Appl	11, Appl	7983, Ap	25195, A	7116, Ap	43443, A	11474, A	58539, A	24969, A	•	4 - 4 - 1

## ALIGNMENTS

US-09-347-833-6

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APPLICANT: GARY BECTON et. al
APPLICANT: GARY BECTON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELI-
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTIC
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9271
LENGTH: 650
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Famodu, Layo O.
APPLICANT: Odell, Joan T.
APPLICANT: Odell, Joan T.
TITLE OF INVENTION: Factors Involved in Gene Expression
FILE REFERENCE: BB-1172
CURRENT APPLICATION NUMBER: US/09/347,833
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,415
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
LENGTH 428
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Best Local Similarity
Matches 7; Conserve
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Patent No. 6294658
GENERAL INFORMATION:
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TYPE: PRT
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RESULT 5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6451
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; ORGANISM: Oryza sativa
US-09-347-833-4
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Sequence 22566, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
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SOFTWARE: Patent.pm
SEQ ID NO 6451
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Patent No. 663906
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SEQ ID NO 4
LENGTH: 655
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
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EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 11
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APPLICANT: Odell, Joan T.
TITLE OF INVENTION: Factors Involved in Gene Expression
FILE REFERENCE: BB-1172
FILE REFERENCE: BB-1172
                                                                                                                                                                                                      local Similarity
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CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22566
ENDTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-513-999C-5651
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Best Local Similarity
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, James E
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS:
TITLE OF INVENTION: USE
FILE REFERENCE: 600-1-29
FILE REFERENCE: 600-1-29
CURRENT APPLICATION NUMBER: US/09/087,465A
CURRENT FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5651
LENCTH: 95
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins Patent, No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5651,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Candida albicans
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                                                                                                                                                                                                                                 22, Application US/09087465A
o. 6160092
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                                             US-09-526-542-6
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US-09-087-465-22
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                                                       SOFTWARE: PatentIn version 3.0

SEQ ID NO 6

SEQ ID NO 6

SEQ ID NO 6

SEQ ID NO 6

TYPE: PRI
TYPE: PRI
ORGANISM: Mouse
PEATURE:
PEATURE:
PEATURE:
NAME/KEY: misc_feature
LOCATION: (2)...(424)
OTHER INFORMATION: note: "SH2 domain of murine STAT3"
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09526542
Patent No. 6369198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 4
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APPLICANT: SERLUPI
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Patent No. 6369198
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CURRENT APPLICATION NUMBER: US/09/526,542
CURRENT FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                             FILE REFERENCE: SERLUPI=2
CURRENT APPLICATION NUMBER: US/09/526,542
CURRENT FILING DATE: 2000-03-19
CURRENT FILING DATE: 19
                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                       APPLICANT: SERLUPI-CRESCENZI, Ottaviano APPLICANT: DELLA PIETRA, Linda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (2)...(424)
OTHER INFORMATION: note: "SH2 domain of the published hSTAT3 sequence (Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 107
TYPE: PRT
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les 6; Conserva
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VENTION: ALLELIC VARIANTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERLUPI-CRESCENZI, Ottaviano
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14.6%;
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100.0%; Pred. No. 48;
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 Score 6; |
Pred. No.
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               Length 141;
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US-10-117-087-6
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APPLICANT: SERLUPI-CRESCENZI, Ottaviano
APPLICANT: DELLA PIETRA, Linda
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
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                                           Matches
                                                       Query Match
Best Local
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Best Local (
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CURRENT FILING DATE: 2002-04-08
PRIOR PPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/117,087
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US/09/526,542
PRIOR FILING DATE: 2000-03-19
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3 FILE REFERENCE: SERLUPI=2
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APPLICANT: DELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN
                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(424)
OTHER INFORMATION: note:
                                                                                                                                                                     TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (2).7.424)
OTHER INFORMATION: note: "SH2 domain of the published hSTAT3 sequence OTHER INFORMATION: (Akira et al.)
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ORGANISM: Human
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nes 6; Conserv
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25 FISKER 30
14 FISKER 19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
                                                                                                                                                                                                                                                                                tent No. 5820862
                                              APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
                                   CORRESPONDENCE ADDRESS
                                                                                                                                APPLICANT:
                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, Jacqueline E.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg, Stanley M.
TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Gene
TITLE OF INVENTION: and Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/05741
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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: IMMULOGIC PHARMACEUTICAL CORPORATION 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                Application US/08482142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Christensen O'Connor Johnson Kindness
1420 Fifth Avenue, Suite 2800
                                                                                                                              Chen, Xian
Evans, Sean
                                                                                                                                                                                                      Greenstein, Julia
Kuo, Mei-chang
                                                                                                                                                                 Franzen, Henry
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100.0%; Pi
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100.0%; Pred. No. 54;
tive 0; Mismatches
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o. 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-482-142-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 193,
Patent No. 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          APPLICANT: C.C.,
APPLICANT: Evans,
APPLICANT: Evans,
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
TITLE OF INVENTION: 207
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY AGENT INFORMATION:
             APPLICATION NUMBER: US/08/478,572 FILING DATE: 07-June-1995 CLASSIFICATION:
                                                                                                                                                             COUNTRY: US
ZIP: 02154
                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 6; Conserv
                                                                                                                                                                                                             CITY: WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 LVDQLE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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Chen, Xian
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Kuo, Mei-chang
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APPLICATION NUMBER: 08/445,307 FILING DATE:

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; LENGTH: 181 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-572-193
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; Sequence 193, A
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION UNMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELEPHONE: (617) 466-6040
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
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NAME: CRAIG, ANNE I.

REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEPHAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 antino acids
TYDE, saits acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No. 626849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITODES OF THE MAJOR ALLERGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
COUNTRY: US
ZIP: 02154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 610 LI
CITY: WALTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 LYDOLE 32
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Kuo, Mei-chang
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Franzen, Henry
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o. 60;
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; MOLECULE TYPE: protein
US-08-484-296-193

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 27 LVDQLE 32
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Db 72 LVDQLE 77

Search completed: February 1, 2005, 15:35:45
Job time: 18.5556 secs
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Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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Published Applications AA:*

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2: /cgn2-6/ptodate/1/pubpaa/US06 NEW PUB.pep:*

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12: /cgn2-6/ptodate/1/pubpaa/US09 PUBCOMB.pep:*

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16: /cgn2-6/ptodate/1/pubpaa/US10B PUBCOMB.pep:*

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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
8 6 6 6 7 7 7 7 7 7 7 7 9 0	Score
177.1 177.1 177.1 177.1 177.1 144.1 166.6	Query Match 1
111 53 3238 406 6633 406 45 45	Query Match Length DB
15 15 15 16 16 16 17	8
US-10-128-558-167 US-10-424-599-275868 US-10-767-701-41775 US-10-437-963-187132 US-10-424-599-149524 US-10-425-114-53502 US-10-437-963-110339 US-10-437-963-110342 US-10-437-963-110342 US-10-427-963-110342 US-10-427-963-110342 US-10-427-963-110342 US-10-427-963-110342 US-10-424-599-149522 US-09-864-761-44493 US-10-425-115-340619 US-09-989-920-197	ID
Sequence 167, App Sequence 275868, Sequence 41775, A Sequence 187132, Sequence 189524, Sequence 53502, A Sequence 110339, Sequence 151847, Sequence 110342, Sequence 149522, Sequence 149522, Sequence 44493, A Sequence 340619, Sequence 340619,	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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144	141	141	141	140	140	138	128	122	119	118	117	114	112	105	105	103	100	98	97	95	87	83	83	74	73	72	71	61	5 5	52	51
16	16	14	14	16	15	15	17	17	17	16	17	16	17	16	15	15	16	17	16	17	16	17	9	17	17	16	15	15	17	14	15
-10-437-9	7-963-	-10-117-087-	-117-087-	0-437-	-10-425-114-4	-10-424-	-10-425-115-2	-425-	-10-425-115-	US-10-437-963-148111	-10-425-115-	-10-437-963-11244	0-425-115-21936	.963	-599-2713	-599-20586	-963-13798	115	-963-18073	·115-3	-701-5432	·115	64-761-35	-10-425-115-36411	-10-425-115-	-10-437-963-	-10-282-	4-599-24564	-10-425-115-2	US-10-029-386-29247	0-424-599-2
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145920,	102617,	Appl	4, Appli	g	41418, A	280443,	σ	294217,	0	148111,	266857,	112442,	219369,	141966,	271306,	205861,	137984,	332775,	180730,	341629,	54325, A	295263,	5244, A	364110,	266081,	178932,	68905, A	245649,	203297,	9247	19715,

## ALIGNMENTS

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Remai	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	CURRE	CURRE	FILE	TITLE	TITLE	APPLI	APPLI	APPLI	APPLI	APPLI	GENERA	Public	Sequen	RESULT 1 US-10-12
FILING DATE: 2000-02-28 ning Prior Application data removed - See File Wrapper or		FILING DATE	APPLICATION N	PRIOR FILING DATE: 2000-04-27		PRIOR FILING DATE: 2000-02-03	PRIOR APPLICATION NUMBER: US 09/496,914	RIOR FILING DATE: 2001-01-25	PRIOR APPLICATION NUMBER: PCT/US01/02623	FILING DATE	PRIOR APPLICATION NUMBER: US 09/491,404	•		FILING DATE		FILING DATE	PRIOR APPLICATION NUMBER: US 09/488,725	FILING DATE		CURRENT FILING DATE: 2002-04-22	CURRENT APPLICATION NUMBER: US/10/128,558	FILE REFERENCE: 812A	TITLE OF INVENTION: Polypeptides	OF INVENTION: N	APPLICANT: Drmanac, Radoje T	APPLICANT: Boyle, Bryan J	APPLICANT: Weng, Gezhi	APPLICANT: Wang, Zhiwei	APPLICANT: Tang, Y. Tom	GENERAL INFORMATION:	Publication No. US20040219521A1	Sequence 167, Application US/10128558	RESULT 1 US-10-128-558-167
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PALM.																																	

; TYPE: PRT ; ORGANISM: Homo sapiens US-10-128-558-167

SOFTWARE: pt\_FI SEQ ID NO 167 LENGTH: 1149

NUMBER OF SEQ ID NOS:

\_FL\_genes Version 6.0

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US-10-767-701-41775; Sequence 41775, Application US/10767701; Publication No. US20040172684A1; GENERAL INFORMATION:
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                                                     ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C6863_1.pep
US-10-767-701-41775
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US-10-424-599-275868
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Best Local Similarity
Matches 20; Conserva
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Best Local Similarity
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SEQ ID NO 41775
LENGTH: 238
TYPE: PRT
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LENGTH: 53
TYPE: PRT
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                                                                                                                                                                                                APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                           APPLICANT: Kovalic, APPLICANT: Zhou, Y APPLICANT: Cao, Yo
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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                                                                                         ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_91128C.1.pep
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17.1%;
100.0%;
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100.0%; Pred. No.
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Score 7;
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o. 9.4;
DB 16;
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3.2e-12;
             Length 238;
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE REFERENCE: 38-21(53221)B CURRENT FILLS APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-55-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 187132 LENGTH: 314 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-10-424-599-149524
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_106042C.1.pep
US-10-424-599-149524
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_83866C.1.pep
US-10-437-963-187132
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                                                                                                                                                           NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 149524
LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                           Sequence 149524, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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Publication No. US20040123343A1
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                                       NAME/KEY: unsure
LOCATION: (1)..(349)
OTHER INFORMATION: unsure at all Xaa locations
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LOCATION: (1)..(314)
OTHER INFORMATION: unsure at all Xaa locations
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                                   FEATURE:
                                                                                                          FEATURE:
                                                                                                                         ORGANISM: Glycine
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; OTHER INFORMATION: Clone ID: 701129526_FLI.pep
US-10-425-114-53502
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US-10-425-114-53502
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                                                   US-10-437-963-110339
                                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53502
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 110339, Application US/10437963 Publication No. US20040123343A1
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Best Local Similarity
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Best Local
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 Best Local Similarity
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
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                                                                                            LENGTH: 633
TYPB: PRT
ORGANISM: Oryza Bativa
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TYPE: PRT
ORGANISM: Glycine max
                                                            FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_14411C.1.pep
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Screen, Steven E
Tabaska, Jack E
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Barbazuk, Brad
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17.1%;
100.0%;
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 Score 7; Pred. No.
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o. 58;
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Sequence 151847, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_14414C.1.pep
US-10-437-963-110342
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US-10-437-963-151847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-437-963-110342
                                                                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 110342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 15.1847

LENGTH: 660
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Best Local :
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                 ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                    TYPE: PRT
                                                                                                                                                                  LENGTH: 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               588 PLVDQLE 594
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7; Conservative (
                                                                                                                                                                                                                                                                                                                                                           Zhou, III...
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Wu, Wei
                                                                                                                                                                                                                                                                                                      Li, Ping
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Barbazuk, Brad
            17.1%; Score 7; DB ilarity 100.0%; Pred. No. 90 Conservative 0; Mismatches
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                               DB 16;
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5. 90;
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                                               Length 662;
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US-10-424-599-149522
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Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
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APPLICANT: Kovalic David K
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NPPLICANT: Rank, David R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(665)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
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                                                 IOR APPLICATION NUMBER: US 60/207,456
IOR FILING DATE: 2000-05-26
IOR APPLICATION NUMBER: US 09/632,366
IOR APPLICATION NUMBER: US 09/632,366
IOR APPLICATION NUMBER: GB 24263.6
IOR FILING DATE: 2000-10-04
IOR APPLICATION NUMBER: US 60/236,359
IOR FILING DATE: 2000-09-27
IOR APPLICATION NUMBER: PCT/US01/00666
IOR FILING DATE: 2001-01-30
IOR APPLICATION NUMBER: PCT/US01/00667
IOR APPLICATION NUMBER: PCT/US01/00667
IOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/180,312 FILING DATE: 2000-02-04
APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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5. US20020048763A1
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Chen, Wensheng
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                                      2001-01-30
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b; Pred. No. 90;
0; Mismatches
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Query Match
Best Local Similarity
Tatches 6; Conserve
                                                                      ; OTHER INFORMATION: Clone ID: MRT4577_73815C.1.pep US-10-425-115-340619
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                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 340619
LENGTH: 45
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Publication No. US20040214272A1
GENERAL INFORMATION:
                    Query Match
Best Local (
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                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
                                                                                                       TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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FILING DATE: 2001-01-29
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INFORMATION:
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 Similarity 6; Conserv
 ilarity 100.0%; | Conservative 0;
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EXPRESSED
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14.6%; Score 6; DB
100.0%; Pred. No. 91
ive 0; Mismatches
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IN FETAL LIVER, SIGNAL =
IN BRAIN, SIGNAL = 0.86
IN LUNG, SIGNAL = 1
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Pred. No. 75;
0; Mismatches
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                                  DB 17;
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SIGNAL = 0.86
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                                  Length 45
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US-10-029-386-29247

; Sequence 29247, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:
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US-10-424-599-219715
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 219715
LENGTH: 51
TYPE: PRT
ORGANISM: Glycine max
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and ProteILE REFERENCE: DEX-0291
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER: OF SEQ ID NOS: 284
SOCTWARE: Patentin version 3.1
SEQ ID NO 197
LENGTH: 48
TYPE: DET
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                      37 LENRLG 42
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                                                                             Query Match
Best Local Similarity
watches 6; Conserva
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HONAID GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29247
LENGTH: 52
TYPE: PRT
                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO CHR17.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: SWISSPROT HIT: P52631, EVALUE 1.00e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                               14 FISKER 19
FISKER 14
                                                                                                         Conservative
                                                                                                                                  100.0%;
                                                                                                    14.6%; Score 6; DB 14; Length 52; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                1e+02;
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Search completed: February 1, 2005, 15:44:52 Job time: 61.7778 secs This Page Blank (uspto)

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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A42929
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291.016 Million cell updates/sec
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Query Match 17.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 7.3; Matches 7; Conservative 0; Mismatches	AG3305 AG3305 AG3305 C;Species: Brucella melitensis C;Species: Brucella melitensis C;Accession: AG3305 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Pat.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative int A;Reference number: AD3252; PMID:11756688 A;Accession: AG3305 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-276 <kur> A;Cross-references: UNIPROT:Q8FIL5; UNIPROT:Q8FZA1; A;Experimental source: strain 16M C;Genetics: A;Genetics: A;Genetics: A;Genetics: methyltransferase</kur>	0%; Pred. No. 6.3 0; Mismatches	/Stallin Bl protein - zebra fish ss: Brachydanio rerio (zebra fish) 09-Nov-2001 #sequence_revision 09-Nov-2001 jion: JC7706 J.Y.; Chang, B.E.; Chen, Y.H.; Lin, C.J.F. Biophys. Res. Commun. 285, 105-110, 2001 : Molecular cloning, developmental expressionce number: JC7706; MUID:21331298; PMID:11 sion: JC7706 lle type: mRNA les: 1-232 cCHE> references: UNIFROT:090WT1; GB:AJ317957 nt: This protein is involved in regulation family: beta-crystallin /Region: active proline- and alanine-rich not the state of the st	ALIGNMENTS	30 6 14.6 283 2 H97610 31 6 14.6 295 2 D90252 32 6 14.6 302 2 T08522 33 6 14.6 302 2 S32178 34 6 14.6 302 2 S70151 35 6 14.6 317 2 G83593 36 14.6 326 2 AB1169 37 6 14.6 326 2 AB1169 39 6 14.6 333 2 G95380 39 6 14.6 333 2 G95380 40 6 14.6 336 2 T50935 41 6 14.6 337 2 F97427 42 6 14.6 347 2 F97427 42 6 14.6 350 2 C91014 43 6 14.6 350 2 E85858 44 6 14.6 350 2 H64988 45 6 14.6 351 2 H70619
Length 276; 0; Indels 0; Gaps 0;	[imported] - Brucella melitensis (strai: 02 #text_change 09-Jul-2004 Patra, G.; Mujer, C.; Los, T.; Ivanova, H.; Hagius, S.; O'Callaghan, D.; Letessintracellular pathogen Brucella melitens	0; Indels 0; Gaps 0;	<pre>L #text_change 09-Jul-2004 ; Wu, J.L.; Kuo, C.M. ton, and hormonal regulation of zebrafi [437379 by growth factors. notif #status predicted Length 232;</pre>		hypothetical prote conserved hypothet NTP-binding protei trnsC protein homol glutathione synthe hypothetical prote hypothetical prote probable periplasm isomerase/decarbox flagellar motor sw flagellar motor sw hypothetical prote probable subunit o cytochrome c-type hypothetical prote

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N;Alternate names: poly(A)-binding protein
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Le, H.; Chang, S.C.; Tanguay, R.L.; Gallie, D.R. Bur. J. Biochem. 243, 350-357, 1997
A;Title: The wheat poly(A)-binding protein function A;Reference number: Z12044; MUID:97182620; PMID:90
                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P93616; EMBL:U81318; NID:g1737491; PIDN:AAB38974.1; PID:g173
A;Experimental source: sprout tips from 5 day old growing sprouts
                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-651 <LEH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-584 < SHE>
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A;Title: Splicing of a group II intron in a functional transfer A;Reference number: S77646; MUID:97000348; PMID:8843433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mobilisation protein A - Lactococcus lactis self-transfer sex factor C;Species: Lactococcus lactis C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000 C;Accession: S77647
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                                                                                                                                                                             ;121-187/Domain: ribonucleoprotein repeat homology <RRM2>;212-278/Domain: ribonucleoprotein repeat homology <RRM3>;315-381/Domain: ribonucleoprotein repeat homology <RRM4>
                                                                                                                                                                                                                                                Keywords: nucleus; RNA binding
                                                                                                                                                                                                                                                                                   Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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                                                                                                                     Local Similarity
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100.0%; Pred. No.
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cive 0; Mismatches
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                                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E70385
A; Experimental source: C; Genetics:
                                                            A; Molecule type: DNA
A; Residues: 1-165 < AQF>
                                                                                                 A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                               Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                              conserved hypothetical protein aq_987 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: E70385
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                                    A; Cross-references: UNIPROT: 067112; GB: AE000717; NID: g2983492;
                                                                                                                                                                                                                                       R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young,
                                                                                                                                                                                                                                                                                                                                                        E70385
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D39384
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aq\_987

strain

VF5

₩.G.;

Lenox,

A.L.; Graham,

Ö

. B. 940

Aquifex aeolicus

translation

not shown

PIDN: AAC07079.1;

PID: 92981

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A;Cross-references: GB:M61869; NID:g184449; PID:g184450
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <BEL>
                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #text_change 08-Dec-2000
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000
C;Accession: D39384
R;Bellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991
A;Title: The evolutionarily conserved Krueppel-associated box domain defines a subfamily A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Accession: D39384
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A21851
22K factor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-38 <DAM>
                                                                                                                                                                                                                                                                                                                                                                                                                          finger protein HTF6 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 314, 266-268, 1985
A;Title: Homogeneous interferon-inducing 22K factor is related to endogenous pyrogen and A;Reference number: A21851; MUID:85163727; PMID:3920526
A;Accession: A21851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22K tactor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Sep-1957 #sequence_revision
                                                                          Matches
                                                                                            Query Match
Best Local
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                                   5 KIFLFD 10
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KIFLFD
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100.0%; Pred. No. 16;
tive 0; Mismatches
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; Pred. No.
                                                                        Mismatches
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. 16;
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RESULT 10
F90919
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A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294, 849-852, 2001
A; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Me A; Authbors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Me ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein b2612 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G65039
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A,Cross-references: GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAC75661.1; PID:g1788965
A,Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription regulator TetR/AcrR family homolog lin0845 [imported] - Listeria
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  repressor for uid operon [imported] -
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A; Residues: 1-184 <GLA>
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;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
;Accession: AE1538
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llarity 100.0%; Pred. No. 54
Conservative 0; Mismatches
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100.0%; Pred. No. 60
tive 0; Mismatches
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100.0%; Pred. N
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  Escherichia coli (strain O157:H7, substrain RIMD
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    a
A;Cross-references: UNIPROT:Q59431; GB:AE000257; GB:U00096; NID:g1787898; PIDN:AAC74690
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-196 <HAY'>
A;Crose-references: UNIPROT:Q59431; GB:BA000007; PIDN:BAB35749.1; PID:g13361793; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90919
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A,Reference number: A99629; MUID:21156231; PMID:11258796
A,Accession: F90919
                                                                                                                                                                                  glucuronide repressor gusR - Escherichia coli (strain K-12) C;Species: Escherichia coli (C;Decies: Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change C;Accession: D64918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: C85768
C;Accession: C85768
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glass
R;Perna, N.T.; Dimalanta, N.W.; Lim, A.; Dimalanta,
                                                        Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Raference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repressor for uid operon [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
A; Molecule type: DNA
A; Residues: 1-196 <BLAT>
                                       A;Status: nucleic acid sequence
                                                                                                                                          R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: ECs2326
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Best Local
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A; Gene: CC0375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein CC0375 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: gusR; uidR
C;Function:
A;Description: repressor of uidRABC (= gusRABC) operon
C;Keywords: transcription remulation
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;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
;Accession: A5926; Levy, S.
;Todd, S.C.; Doctor, V.S.; Levy, S.
;tochin. Biophys. Acta 1399, 101-104, 1998
;Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
;Reference number: A59258; MUID:98390278; PMID:9714763
;Accession: A59263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etraspan TSPAN-2 - human
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Best Local
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Gene: TSPAN-2
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Residues: 1-222 <TOD>
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Residues: 1-204 <STO>
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F;77-80/Domain: intracellular #status predicted <CY2>
F;81-109/Domain: transmembrane #status predicted <TW3>
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A;Experimental source: ocular ciliary epithelial cell
C;Superfamily: CD9 antigen
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A; Residues: 1-226 < MAR>
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J. Blochem. 112, 63-67, 1992
A;Title: Molecular cloning of the bovine CD9 antigen from ocular ciliary epithelial cells.
A;Reference number: JX0221; MUID:93054422; PMID:1339429
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C;Date: 09-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: JX0221
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',119-219/Domain: transmembrane #status predicted <TM4>
',220-226/Domain: intracellular #status predicted <CY3>
',520-256/Domain: intracellular #status predicted <CY3>
',50/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Q704w2 bos taurus

Q88fe3 Q7rq16 Q7m4s7

3 pseudomonas 6 plasmodium 7 homo sapien

Bac92404 oryza sat Bac92537 oryza sat Q6yyv1 oryza sativ Bad16229 oryza sat

Q9at32 daucus caro Q6z050 oryza sativ

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Q7T153
Q7T152
Q7SY48
EX7S_VIBPA
EX7S_VIBVU
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Q8N7L7
BP28_MACFA
BP28_HUMAN
Q8VCK1
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Q6P197
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Q8fza1 brucella su
Q8fyl15 brucella me
Q6mz13 methylocyst
Cae48356 methylocy
Q7ma16 wolinella s
Q8dkq2 synechococc
Q9m6e4 nicotiana t
Q8ky20 uncultured
Q48722 lactococcus
Q48665 lactococcus
Q48665 lactococcus
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Q6p197 homo sapien
Aah65205 homo sapien
Q8n717 homo sapien
Q9m44 macaca fasc
Q9m583 homo sapien
Q8vck1 mus musculu
Q8cct5 mus musculu
Q7t153 brachydanio
Q7t152 brachydanio
Q7t152 brachydanio
Q7t152 brachydanio
Q87t16 vibrio vuln
Q8m17 vibrio vuln
Q9mt1 brachydanio
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sheemen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gybs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Kones S. T. Mayra M.A.
                                                                                                                                                 Matches
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Best Local
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Q96ES5,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
FLJ10359 protein.
RAME=FLJ10359;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2001) to the EMI
EMBL; BC011983; AAH11983.1; -.
InterPro; IPR008938; ARM.
SEQUENCE 349 AA; 39921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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       NCLYKIFLFDTQHFISKERAGALMMPLVDQLENRLGGEEKF 41
                                                                                                                                                 Conservative
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Q62050
BAC92404
BAC92537
Q6YYV1
BAD16229
Q8BFE3
Q7RQ16
Q7M4S7
Q9QVR3
Q9QVR4
Q6JUU6
AAR23946
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                                                                                                                                                 Mismatches
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Score

Length DB

1106 1106 1106 897 958 2144 349 408 1278 1336 2159

Query Match

Indels

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Gaps

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Minimum Maximum

DB seq length: 21
DB seq length: 2000000000

Database :

Pred. No. score grea and is der

Total number of hits satisfying

Word size : Searched:

> 1825181 seqs, Gapop 60.0 , OFIGO

Scoring table: Sequence: Title: Perfect score:

SEQ5GLY2017

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Copyright

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RESULT 3
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.R.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Bistepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stepleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A A Jones S.J., Marra M.A.,

A Jones S.J., Marra M.A.,
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Best Local :
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE FROM N.A.
TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; Peingold E.A., Grouse L.H., Derge
                         SEQUENCE FROM N.A.
                                                                                                                                                                                           FLJ10359 protein (Fragment) FLJ10359.
                                                                           NCBI_TaxID=9606;
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Submitted (JAN-2004) to t
EMBL; BC065205; AAH65205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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Mammalia; Eutheria;
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                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Pred. No. 3.4e-35;
; Mismatches 0;
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RRA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Marakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Abe K., Kamihara K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Takabashi F., Yosida M., Hotuta T., Kusano J.,
Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shimizu F., Wakebe H.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
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Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farme R.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Q8N7L7;
01-OCT-2002 (
01-OCT-2002 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein FLJ40893.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BO
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Ota T., Suzuki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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"Generation and initial analysis
and mouse cDNA sequences"
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c. Natl. Acad. Sci. U.S.A.
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
Pred. No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamazaki M., Y
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                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrate by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                     NON TER
                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae;
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                                                                                                       SEQUENCE
                                                                                                                                                                                        EMBL; AB049842; BAB16728.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=BAP28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein BAP28 (QnpA-17571) (Fragment).
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Q9GM44;
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                                                                                                                                                              InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
                                                                                                                                                                                                                                                                                                                                                                                     ibraries."
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                                             20;
                                                           Similarity
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NCLYKIFLFDTQHFISKERA 20
                                                                                                                                      PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCLYKIFLFDTQHFISKERAGALMMPLVDQL 780
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                                                                                                    920
958 AA;
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                                            48.8%;
larity 100.0%
Conservative
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                                                                                                                     956
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                                                                                                    108644 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958
                                                                                                                                                                                                                                   moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                         DB 1;
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                                                           1.2e-12;
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                                                                       Length 958;
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamateu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Isono Y., Makamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kahu Y., Kodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Kahu Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Takahashi F.Jjii A., Hara H., Tanae T.-O.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanaee T.-O.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanaee T.-O.,
RA Momura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Momiya S., Momiyama H., Satoh N., Takami S., Terashima Y., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Makagawa S., Senoh A., Mizoyuchi H., Goto Y., Shimizu F., Wakebe H.,
RA Mishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Makagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,
RA Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Watanabe T., Satoh T., Shirai Y., Masahita R.,
RA Nakai R., Watanaba T., Nakamura Y., Oha
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Q9H583; Q9NW23;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
05-JUL-2004 (Rel. 4
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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=14702039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel BAP28 gene and I
Patent number WO0100669,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bougueleret L.,
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AL136105;
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    CAC26776.1;
CAC15948.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOI=10.1038/ng1285;
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, 04-JAN-2001.
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annotation updat
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XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Foshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Dickson M.C.,

XX Allalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

XX Allalon D.K., Salska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Allalon D.K., Malek U., Smailus D.E., Schnerch A., Schein J.E.,

XX Allalon D.K., Malek U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                EMBL:
                                                 Submitted
                                                            Strausberg R.;
                                                                                               STRAIN=mix FVB/N;
                                                                                                                                      "Generation and initial analysis of more and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16
                                                                            TISSUE=Mammary tumor.
                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=mix FVB/N;
TISSUE=Mammary tumor.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=BC019693;
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SWISS-2DPAGE, Q9H583; HUMAN.
InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
                                                                                                                                                                                       Jones S.J., Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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; BC019693; AAH19693.1; MGI:2384983; BC019693. rPro; IPR008938; ARM.
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Rodentia;
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                                                                         WAP-TGF alpha model. 7 months old,
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Last annotation update)
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Pred. No.
                                                                                                                                       99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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V; D66816EE78D8C9B7
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Best Local S
Matches 18
                                                        MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUB=Olfactory brain;
MEDLINE=2049374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8CCT5
Q8CCT5;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last anotation update)
01-MAR-2004 (TrEMBLrel. 26, Last anotation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430400D06 product:hypothetical ARM reps
structure containing protein, full insert sequence.
 SEQUENCE FROM
                                               sequencing
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                Genome Res.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Olfactory brain;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                          Nature
                                                                                                                                                                                                                                                                                                                                                                                                                             60,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Olfactory brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium;
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MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=BC019693;
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                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs.
420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                            pipeline with 384 multicapillary
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                              10:1757-1771 (2000)
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N.A.
                                                                                                                                                                                                            TISSUE=Olfactory brain;
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Pred. No.
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           Q7T152

Q7T152;

PRELIMINARY;

PRT; 1336 AA.

Q7T152;

01-OCT-2003 (TrEMBLrel. 25, Created)

01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

S1:ZC146F4.2.1 (Novel protein similar to human BAP28) (Fragment).

Name=S1:ZC146F4.2;

Name=S1:ZC146F4.2;

Parachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes,

Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garner P.;
Garner P.;
Submitted (JUL-2003) to the
Submitted (JUL-2003) to the
EMBL; AL732629; CAE17602.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7T153;
Q7T153;
01-OCT-2003
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SI:zC146F4.2.2 (Novel protein similar to human BAP28) (Fragment)
Name=SI:zC146F4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish)
Eukaryota, Metazoa, Chordata,
Actinopterygii, Neopterygii,
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NCBI_TaxID=7955;
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SEQUENCE 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Gudin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Bonaldo M.F., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Madan A., Rodrigues S., Sanchez A.,
Raha S.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Raha Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Raha Jakes R.J., Malsk U., Smailus D.E., Schnerch A., Schein J.E.,
Raha Jakes R.J., Malsk U., Smailus D.E., Schnerch A., Schein J.E.,
Raha Jakes R.J., Malsk U., Smailus D.E., Schnerch A., Schein J.E.,
Raha Jakes R.J., Malsk U., Smailus D.E., Schnerch A., Schein J.E.,
Raha Jakes R.J., Malsk U., Smailus D.E., Schnerch A., Schein J.E.,
Raha Jakes R.J., Malsk U., Smailus D.E., Schnerch A., Schein J.E.,
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                        Submitted (JUL-2003) to the EMBL; BC055128; AAH55128.1; Hypothetical protein. SEQUENCE 2159 AA; 242048
                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q75Y48
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2037
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Pred. No. 13;
0; Mismatches
                                                                                                                                        Score 8;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length human
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EX7S_VIBPA
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EMBL; AP005075; BAC58951.1; -.

EMBL; AP005075; BAC58951.1; -.

I HAMAP; MF 00337; -; 1.

R InterPro; IPR003761; Exonuc_VII_S.

R InterPro; IPR003761; Exonuc_VII_S.

R Pfam; PF02609; Exonuc_VII_S; 1.

R Pfam; PF02609; Exonuc_VII_S; 1.

R Pfam; PF02609; Exonuc_VII_S; 1.

R Pfam; PF02609; Exonuc_VII_S; 1.
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X MEDIINE=22508454; PubMed=12620739;

X MEDIINE=22508454; PubMed=12620739;

X Makino K., Oshima K., Kurokawa K., Yokoyama K., Kubota Y., Kimura S.,

X Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

I distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

C -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large

acid-insoluble oligonucleotides, which are then degraded further

into small acid-soluble oligonucleotides (By similarity).

C -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-

C -1- SIRRINIT. Hetersoligonucleoside 5'-phosphates.
                                                                                                                                        Q8DFA5;
10-OCT-2003
10-OCT-2003
                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Probable exodeoxyribonuclease VII small sub
(Exonuclease VII small subunit).
Name=xseB, OrderedLocusNames=VV10313;
Vibrio vulnificus.
                            Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                        EX7S
                                                                                                                                                                                                          DABIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
55-JUL-2004 (Rel. 44, Last anno
Probable exodeoxyribamas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EX7S VIBPA
Q87RT8;
10-OCT-2003
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
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Name=xseB; OrderedLocusNames=VP0688;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the xseB family.
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100.0%; Pr
                                         Gammaproteobacteria;
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Pred. No.
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F6A CRC64;
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                                                                                                                                                                                                                                                                                                                                                            Length 80;
                                         Vibrionales;
                                                                                                        (E)
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                                                                                                        3.1.11.6)
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RESULT
Q7MN47
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EMBL; AP005333; BAC93334.1; -.

GO; GO:0009318; C:exodeoxyribonuclease VII

GO; GO:0009855; F:exodeoxyribonuclease VII

GO; GO:0004527; F:exonuclease activity; IE

GO; GO:0004527; F:exonuclease activity; IE

GO; GO:0006308; P:DNA catabolism; IEA.

R InterPro; IPR003761; Exonuc VII S.

R Pfam; PF02609; Exonuc VII S; 1.

R ProDom; PD028235; Exonuc VII S; 1.

R ProDom; PD028235; Exonuc VII S; 1.
                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Cre
01-MAR-2004 (TrEMBLrel. 26, Las)
01-MAR-2004 (TrEMBLrel. 26, Last
Exonuclease VII small subunit.
Name=VV0870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                 PubMed=14656965, Chang Y.-C., Chang C.-H., Tsai FubMed=14656965, Chang Y.-C., Chang C.-H., Tsai Fuiao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J. Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F., "Comparative genome analysis of Vibrio vulnificus, a
                                                                                                                                                                                                                                                                                                                                                      Q7MN47
Q7MN47;
01-MAR-2004
                                                                                                                         "Comparative genome analysis of pathogen."; Genome Res. 13:2577-2587(2003).
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
SEQUENCE
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    Vibrio vulnificus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhee J.H.,
Choy H.E.;
                                                                                                                                                                                                                                                NCBI_TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP: MF_00337; -; 1.
InterPro; IPR03761; Exonuc_VII_S;
Pfam; PF02609; Exonuc_VII_S; 1.
TIGRPAMs; TIGR01280; xseB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE016798; AA008843.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Submitted (DEC-2002) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM STRAIN=CMCP6;
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8756 MW; FE23B015BD49F5ED CRC64;
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Gammaproteobacteria; Vibrionales;
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Last annotation update)
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Pred. No
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o. 18;
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                                                                                 VII complex; IEA.
VII activity; IEA
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Search completed: February 1, 2005, 15:31:06 Job time: 72.5556 secs
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Q90WT1
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                                                                                                                                                                                                                                                                                                                                                                                                       the vertebrate eye lens (By similarity).

C -| DOMAIN: Has a two-domain beta-structure, folded into four very similar greek key motifs (By similarity).

C -|- SIMILARITY: Belongs to the beta/gamma-crystallin family.

BENEL; AJ317957; CAC84899.1; -.

REMEL; AJ317957; CAC84899.1; -.

REMEL; AJ317957; CAC84899.1; -.

RESP; P26775; 1BD7.

RESP; P26775; 1BD7.

REFN; ZDB-GENE-010813-1; crybb1.

RICTPO; IPRO11064; Crystallin.

RICTPO; IPRO11024; G crystallin.

RICTPO; IPRO11024; G crystallin.

REFN; EN00247; XTALDS; 2.

REMEL; SM00247; XTALDS; 2.

REMEL; SM00247; XTALDS; 2.

REMEL; SM00247; XTALDS; 2.

REMEL; SM00247; XTALDS; 2.

REMEL; SM00247; XTALDS; 2.

REMEL; SM00247; XTALDS; 2.
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity 100
Matches 7; Conservative
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Name=crybbl; Synonyms=crystallin Bl;
Brachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90WT1 PRELIMINARY; PKT; 232 MA.
Q90WT1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Chen J.Y.;

Thesis (2001), Department of Institute of Zoology, Academia Sinica,

Taipei, Taiwan.

-!- FUNCTION: Crystalling are the dominant structural components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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41 YKIFLFD 47
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                                                                                                                                                                                                                                                                                                                17.1%; Score 7; DB 2; 100.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Length 232;
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                                                                                                                                                                                                                                                                                Gaps
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Post-processing: Listing first 45 summaries
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ABM68350
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ABU24428
ADJ49159
ADJ48818
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ADE08012
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ABB29466
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Abu24428 Protein e
Adj49159 Oil-assoc
Adj4818 Oil-assoc
Adn73151 Thale cre
Abm68350 Photorhab
Adn04625 Antipsori
Aam39043 Human pol
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                               Aam67825
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AAW54099
     20-SEP-1996;
03-APR-1997;
04-APR-1997;
The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, B123, BE2, BE14 BE31 or BE445, or a composition for the detection of a BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BRCA1, useful to identify a patient having, or at risk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the biological activity of the BRCA1-BARD1,
                                                                                                                                                                                             DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - breast cancer antigen, BRCA1, binding proteins are useful to i patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                     WPI; 1998-230317/20.
N-PSDB; AAV24135.
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                                                                                                                                                                    Disclosure; Page 287-288; 348pp; English.
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Minimum Maximum

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Title:

Run on: OM protein -

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Result No.

Score

	5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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	ABM55182	AAU58663	ABU20127	ADK47657	ABJ10298	AAG01477	ADJ28436	ABU12410	ABB03116	ADC89625	ABG44588	ABG56579	AAM61993	AAM74797	ABB25176	AAM34913	ABB41137	AAM20415	ABG37371	AAM03380
,	Abm55182	Aau58663	Abu20127	Adk47657	Abj10298	Aag01477	Adj28436	Abu12410	Abb03116	Adc89625		Abg56579	Aam61993	Aam74797	Abb25176	Aam34913	Abb41137	Aam20415	Abg37371	0
	Propionib	Propionib	Protein e	Streptoco	Human lun	Human sec	Human mus	Novel hum	Human mus	Human PMS	Human pep	Human liv	Human bra	Human bon	Protein #	Peptide #	Peptide #	Peptide #	Human pep	Peptide #

ALIGNMENTS

### BARD1; ring protein; BRCA1; breast cancer; risk; diagnosis. Homo sapiens BAP28 sequence AAW54099 standard; protein; 515 Baer R; TEXAS SYSTEM. (first entry) 96US-0025296P. 97US-0042611P. 97US-0042985P. 97WO-US016842 ₽

which as identify

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Matches 20; Conserv

Conservative 0;

Pred. No. 6.6e-12; ; Mismatches 0;

Indels

0

Gape

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RESULT 2
ADE08012
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14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372331P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-0376045P.
                        tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
                                                                                                                                                                                                                                                           Ghosh M,
Ma Y, W
                                                             expressed; as molecular weight tags; to identify chromosomes c
                                                                                The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially
                                                                                                                                          Claim 20;
                                                                                                                                                             New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tin which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                     Tang
                                                                                                                                                                                                                        N-PSDB; ADE07101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445, a specific anti-BARD1 antibody can be used to identify a patient having or at risk of developing cancer
                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2001; 2001US-0339739P
11-DEC-2001; 2001US-0339453P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE08012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE08012 standard; protein; 1149
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                                                                                                                                                                                                                                   2003-569235/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LKLLCKNFGAENDDFFVPVLSTAVKLIAPERKEEKNVLGSA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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                                                                                                                                        SEQ ID NO 1078; 1177pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (useful for identifying genetic disorders) #167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; tissue marker; genetic disorder.
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Weng G, Zhou
, Boyle BJ;
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Pred. No. 6.4e-3
                                                                         markers on gels;
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ou P,
                                                                        as chromosome markers or
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Wang Z;
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Query Match

48 . 88

Score

20; ВB

7;

Length 1149;

Query Match Best Local 9 Matches

ch 48.8%; S l Similarity 100.0%; 20; Conservative 0;

Score 20; Pred. No.

DB 4; L 1.1e-11;

Length 2144;

0

Gaps

0

Mismatches

Sequence 2144

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Sequence 1149 AA;

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RESULT 3
AAB85029
ID AAB8
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                        The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polynucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful as diagnostic analysis. The present sequence represents a protein encoded by a first cDNA sequence of the BAP28 gene consisting of the exons 1 to 45
                                                                                                                                                                                                                                                           New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization oppolymerase chain reaction assays.
                                                                                                                                                                                                                             Claim 14; Page 297-304; 349pp; English.
                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF83909, AAF83910.
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                                                                                                                                                                                                                                                                                                                                                                        Barry C,
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18-JAN-2000; 2000US-0176880P
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2017
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	07-JUL-2000; 2000US-0216867 11-JUL-2000; 2000US-0217487 11-JUL-2000; 2000US-0217489 11-JUL-2000; 2000US-0218290 26-JUL-2000; 2000US-0220963 26-JUL-2000; 2000US-0220964 14-JUG-2000; 2000US-0224519 14-AUG-2000; 2000US-0225211 14-AUG-2000; 2000US-0225211 14-AUG-2000; 2000US-0225211 14-AUG-2000; 2000US-0225266 14-AUG-2000; 2000US-0225266 14-AUG-2000; 2000US-0225266 14-AUG-2000; 2000US-0225266 14-AUG-2000; 2000US-0225266 14-AUG-2000; 2000US-0225261 14-AUG-2000; 2000US-0225261 14-AUG-2000; 2000US-02252675	W0200157182-A2.  09-AUG-2001.  17-JAN-2001; 2001WO-US00135  1-JAN-2000; 2000US-019065  04-FEB-2000; 2000US-018635  24-FEB-2000; 2000US-018635  16-MAR-2000; 2000US-018635  16-ARR-2000; 2000US-0190076  18-AFR-2000; 2000US-0190076  18-AFR-2000; 2000US-0205515  07-JUN-2000; 2000US-0205515  07-JUN-2000; 2000US-0215135	Qy 1 LKLLCKNFGAENPDPFVPVL 20
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			08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 26-SEP-2000; 26-SEP-2000; 27-SEP-2000;
4466110 4466110 4492013 4992009 499211 499211 4992114 4992116 54492116 5449216 5449216 5449216 5449216	000US-0241809 000US-0241826 000US-02441826 000US-0246477 000US-0246475 000US-0246476 000US-0246478 000US-0246528 000US-0246525 000US-0246526 000US-0246526	000US-0235836 000US-0236367 000US-0236368 000US-0236369 000US-0236379 000US-0236370 000US-0237037 000US-0237037 000US-0237039 000US-0237039 000US-0237039 000US-0237039 000US-0237039 000US-0237039	000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02: 000US - 02:

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RESULT 5
AAM87229
ID AAM8
XX AAM8
AC AAM8
XX O7-N
XX Humm
XX Humm
XW Cytc
XX SHomm
XX Homm
XX Homm
XX Homm
XX Homm
XX Homm
XX Homm
                                                                                                                                                                                                                                                                                                                                                                                                                    CC AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynuclectides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to Supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the CC nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                      Homo sapiens
                                                                                               Human immune/haematopoietic antigen SEQ ID NO:14822.
                                                                                                                                 07-NOV-2001
                                                                                                                                                               AAM87229;
                                                                                                                                                                                         AAM87229 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 80 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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N-PSDB; AAK64297.
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7; Conserva
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9 PVLSTAV 65
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                                                                                                                                                                                                                                                                                                                               17.1%; Score 7; DB 4; ilarity 100.0%; Pred. No. 24; Conservative 0; Mismatches
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2000US-02492999.
2000US-02493099.
2000US-02503160P.
2000US-0250391P.
2000US-0251988P.
2000US-02567198P.
2000US-02514799.
2000US-0251866P.
2000US-0251866P.
2000US-02518689.
2000US-0251869P.
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2000US-0254097P.
2001US-0259678P.
                                                                                                                             (first entry)
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25-SEP-2000;
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26-SEP-2000;
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30-AUG-2000;
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2000US-0233064P.
2000US-0234065P.
2000US-0234274P.
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2000US-0234997P.
2000US-0235494P.
2000US-0235484P.
2000US-0235884P.
2000US-0235884P.
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2000US-0216890P.
2000US-021749FP.
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2000US-0246527P.
2000US-0246528P.
2000US-0246529P.
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2000US-024647P.
2000US-024647AP.
2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
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2000US-0246611P.
                                  GENOME
                                  SCI
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Ruben SM

New antisense nucleic acids, useful for identifying proteins or screening

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RESULT 6
ABU24428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) cyroteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For ce example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cthat affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) concerts and be used to produce the secreted (I), by inserting the cc nucleic acids into a host cell and culturing the cell to express the crotein. (I) proteins and polynucleotides may be used to prevent, concerts and treat immune/haematopoietic-derived cells. AAK64703 cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cc sequences from the present invention. AAK54942 to AAK54950 and AAM82169 cropresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                           21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                                                                     Wang
Wall
                          WPI; 2003-029926/02.
N-PSDB; ACA28298.
                                                                                                                                                                                                                                                                   03-OCT-2002.
                                                                                                                                                                                                                                                                                                                            Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 14822; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483426/52.
N-PSDB; AAK60010.
                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                             WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU24428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU24428 standard; protein; 308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK54951 to AAK64702 encode the human
                                                                                                                 (ELIT-)
                                                                     ם בֿי
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
                                                                                                               ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                     encoded by Prokaryotic essential gene #9955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKEEKNV 37
                                                                     Zamudio C,
Trawick JD,
                                                                                                                                           ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 7; DB (ilarity 100.0%; Pred. No. 32)
Conservative 0; Mismatches
                                                                     Malone
Carr (
                                                                     ទី្តំ
                                                                     Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune/haematopoietic antigen (I) to AAM91921. (I) have cytostatic
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                                                                     Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                     Zyskind JW;
Xu HH;
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RESULT 7
ADJ49159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated concoding a polypeptide whose expression is inhibited by the antisense conclude or its fragment whose expression is inhibited by the antisense conclude; (5) producing the polypeptide; (6) inhibited by the containing the vector; (3) an isolated (4) antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular compound that influences the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for required for proliferation; (7) identifying a compound that influences the activity of compound that influences the activity of compound that influences the activity of compound that inhibite gene product lies or a gene on which the test compound that inhibite gene product lies or a gene on which the test compound that inhibite proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene compound that inhibite proliferation of an organism acts; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the gene compound that inhibits are useful for colliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational constitution of an organism. The antisense nucleic acids required for cellular proliferation in cells other than s. aureus, S. typhimurium, c. aureus of the printed specification, but was obtained constant directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                     15-MAR-2002; 2002US-0365301P.
26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
                                                                                                                                                              05-FEB-2004
                                                                                                                                                                                                   US2004025202-A1
                                                                                                                                                                                                                                                                                oil-associated
                                                                                                                                                                                                                                                                                                                       Oil-associated
                                                                                                                    14-MAR-2003;
                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 308
(LAUR/) LAURIE C
                                                                                                                                                                                                                                                                                                                                                                                                    ADJ49159
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ49159 standard; protein; 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any one of 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 KNVLGSA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 KNVLGSA 41
                                                                                                                    2003US-00389566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                              gene; transgenic;
                                                                                                                                                                                                                                                                                                                     related protein #659.
                                                                                                                                                                                                                                                                                                                                                             entry)
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Pred. No. 68;
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                                                                                                                                                                                                                                                                            enhanced seed oil; vegetable
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Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transplant seed.

transgenic

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RESULT 8
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Best Local S
Matches 7
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26-JUN-2002; 2002US-0391786P
26-JUN-2002; 2002US-0392018P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                                                                                             (LAUR/)
(RAVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oil-associated
                                                                                                                                       Laurie CC,
                                                                                                                                                                                                              (SAVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2003; 2003US-00389566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oil-associated gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004025202-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic plant seed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; SEQ ID NO 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-142683/14
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(SAVA/)
(LEDE/)
(ROGE/)
                                                                                             2004-142683/14.
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RAVANELLO M.

SAVAGE T.

LEDEAUX J R.
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SAVAGE T.
LEDEAUX J R.
ROGERS J A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                       Savage T,
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                                                                                                                                       Ledeaux JR,
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1e+02;
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Best Local S
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or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis,
                                                                                                                                  This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genom the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid
                                                                                                                                                                                                                                                  Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
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                                                       The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overtexpressing the E2Fa/DPa transcription factor, given in an exemplification of the
response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful fundanceombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicide antibacterials
                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                     WPI; 2003-148459/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; food; gene expression; plant; animal; microorganism; to antibiotic; biopesticide; virulence factor; disease model; plague;
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                                                                                                              The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                           Sequence
                                                                                                                                                                                         Claim 9;
                                                                                                                                                                                                                       New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                                                                                                                                              WPI; 2004-305105/28.
N-PSDB; ADN04624.
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                                                       Score 7; pred. No.
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1544 APERKEE 1550

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Best Loc Matches

Similarity 7; Conserv

ilarity 100.0%; I Conservative 0;

Score 7; DB 4; Pred. No. 5.7 0; Mismatches

DB 4; Length 4618; . 5.7e+02; ches 0; Indels

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Gaps

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Query Match Sequence

4618

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CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the CC encoded polypeptides (AAM36642-AAM42213) with nootropic, CC immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous System, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system disease, such as CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic cand thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC c.N.S disorders. Note: The sequence data for this patent did not form cycles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM39043
                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                   Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 2188; 10078pp; English.
                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peripheral nervous system, neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemostactic; chemokinstic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000;
19-OCT-2000;
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03-AUG-2000;
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DB; AAI58199.
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2000US-00488725,
2000US-00552317,
2000US-00552317,
2000US-006520312,
2000US-00653450,
2000US-00662191,
2000US-00662195,
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Xu C,
c RT,
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Yang Y,
                                                                                                                                                                                                                                                                                                                    for treating disorders such
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Zhang
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RESULT 13
ADL46346
   06-JUN-2002;
01-AUG-2002;
06-NOV-2002;
08-NOV-2002;
24-DEC-2002;
24-DEC-2002;
24-DEC-2002;
27-DEC-2002;
27-DEC-2002;
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08-APR-2002;
09-APR-2002;
The invention relates to isolated, recombinant polypeptides (I) that have at least one activity of specified bacterial enzymes involved in cell membrane biogenesis. (I) are: UDP-N-acetylglucosamine 1-carboxyvinyl transferase-1 of Streptococcus pneumoniae (S.p.), Pseudomonas acruginosa (P.a.) or Staphylococcus aureus (S.a.); CTP:CMP-3-deoxy-D-manno-octulosonate transferase of Escherichia coli (E.c.) or Haemophilus influenzae (H.i.); UDP-N-acetylmuramylalanyl-D-glutamate- 2,6-
                                                                                                                                                                                                          Beattie Virag C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-alanine-D-alanine adding enzyme; D-alanine-D-alanine ligasë;
UDP-N-acetylguyruvoylglucosamine reductase;
UDP-N-acetylglucosamine pyrophosphorylase;
UDP-N-acetylmuramoylalanine-D-glutamate ligase;
DP-N-acetylmuramoylalanine ligase; aspartate semialdehyde dehydrogenase;
UDP-N-acetylmuramoylalanyl-D-glutamate; X-ray diffraction analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epitope; antibacterial;
UDP-N-acetylglucosamine 1-carboxyvinyl transferase-1;
CTP:CMP-3-deoxy-D-manno-octulosonate transferase;
                                                                                                       Disclosure;
                                                                                                                               New recombinant useful for design
                                                                                                                                                                                              Kanagarajah
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31-MAY-2002;
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                                                                                                                                                                    2003-865361/80.
                                                                                                                                                                                            A, Dharamsi A, Vedadi
B, Mansoury K, Ouyang
, Buzadzija K, Pinder B
ajah D, Thalakada R;
                                                                                                                                                                                                                                                           AFFINIUM PHARM INC
                                                                                                                             inant bacterial enzymes involved in designing potential antibacterial a
                                                                                                                                                                                                                                                                                  2002US-0370899P.
2002US-037110FP.
2002US-0371118P.
2002US-0385283P.
2002US-0400348P.
2002US-0400348P.
2002US-0436345P.
2002US-0436345P.
2002US-0436345P.
2002US-0436368P.
2002US-0436889P.
2002US-0436889P.
2002US-0436900P.
2002US-0436900P.
2002US-0436900P.
2002US-0436900P.
                                                                                                       SEQ ID
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                                                                                                       64; 407pp; English
                                                                                                                                                                                                                   Vedadi M,
Ouyang H,
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Vallee F, Richards D, Nethery K;
Alam MZ, Tai M, Canadien V;
                                                                                                                                 agents.
                                                                                                                                             cell membrane biogenesis,
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AAM89273

ID 8273

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ID 8273

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ID 8273

ID 9270

ID 707-NO

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07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000;
19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2001
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17-MAR-2000;
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2000US-0179065P.
2000US-0184664P.
2000US-0184664P.
2000US-0184654P.
2000US-0198123P.
2000US-0199076P.
2000US-0199123P.
2000US-0214886P.
2000US-0216647P.
2000US-0216647P.
2000US-021664P.
2000US-021664P.
2000US-021664P.
2000US-0218290P.
2000US-0218290P.
2000US-0228214P.
2000US-0225214P.
2000US-0225268P.
2000US-0225268P.
2000US-0225247PP.
2000US-0225247PP.
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Pred. No.
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. 89;
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s (E.f.); UDP-N
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2000US-0225758P 2000US-0225759P

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CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cativity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins and polynucleotides may be used to acide may be used to acide may be used to acide the cell to express the correction. (I) proteins and polynucleotides may be used to provent, cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 crepresent the present invention. AAK85492 and AAM82169 crepresent invention. AAK85492 and AAM82169 crepresent invention.
      Matches
                   Query Match
Best Local :
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                   Sequence 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
N-PSDB; AAK62054.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 16866; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                   c acids encoding human immune/hematopoietic antigen polypeptides,
for preventing, diagnosing and/or treating cancers and metastasis.
    6; Conserv
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                                                                   AA;
    Conservative
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2000US-0246611P.
2000US-0246611P.
2000US-024920P.
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2000US-0251869P.
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2000US-0251989P.
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2000US-0251989P.
2000US-0251989P.
2000US-0251989P.
 14.6%; Score 6; DB ...
100.0%; Pred. No. 1...
tive 0; Mismatches
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DB 4; uc...
No. 1.2e+02;
0;
                                Length 32;
      Indels
    <u>,,</u>
      Gaps
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2000US-0233064P.
2000US-0233065P.
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2000US-023499PP.
2000US-023499PP.
2000US-023499P.

2000US-0235834P.
2000US-0236336P.
2000US-0236368P.
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2000US-023703P.
2000US-0241785P.
2000US-0241785P.
2000US-0241786P.
2000US-0241786P.
2000US-0241786P.

08-SEP-2000;

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13-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 20-OCT 2000; 01-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000; 08-NOV 2000;

2000US-0241826P. 2000US-0244617P. 2000US-0246474P.

2000US-0246475P. 2000US-0246476P. 2000US-0246478P. 2000US-0246478P. 2000US-0246523P. 2000US-0246523P. 2000US-0246525P. 2000US-0246525P. 2000US-0246527P.

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Best Local S
Matches 6
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                          Example 4; SEQ ID NO 33460; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                 Penn
                                                                                                                Sequence 42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed probe encoded protein SEQ ID NO: 33460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM73154;
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                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                 SG,
                      17 VPVLST 22
16 VPVLST 21
                                                       Similarity 6; Conserv
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                                                     14.6%; Score 6; DB 4; Length 42; ilarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0; Indels
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                                                       <u>,</u>
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Search completed: February Job time: 73.7778 secs

1, 2005, 15:20:08

OM protein - protein search, using sw model

Run on: February 1, 2005, 14:58:28; Search time 17.5556 Seconds 154.882 Million cell updates/sec alignments)

Perfect score: Title: SEQSSER1694

Scoring table: Sequence: OLIGO 1 LKLLCKNFGAENPDPFVPVL.....TAVKLIAPERKEEKNVLGSA 41

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters:

Maximum BG seq length: 21 seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \* /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
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/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	υī	4	w	N	ᆫ	Result No.
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264	264	253	253	237	226	218	205	176	169	154	154	154	147	135	133	129	127	127	99	99	90	88	87	81	61	51	Length
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US-09-788-657-25	US-09-788-657-24	ភ	US-08-685-992-10	-796A	US-09-248-796A-18711	US-09-710-279-450	US-09-252-991A-26704		-09-248-796A-	US-08-871-161-2	US-08-231-205A-2	US-08-446-908-2	US-09-710-279-1214	US-09-248-796A-22195	US-09-708-200-17	5229115-2	US-09-270-767-53607	US-09-270-767-38390	US-09-270-767-50877	US-09-270-767-35660	US-09-252-991A-21131	US-09-248-796A-25228	US-09-513-999C-4616	US-09-621-976-6450	US-09-583-110-4172	US-09-513-999C-5558	ID
e 25,	(D N)	e 10,	e 10,	e 188:	Sequence 18711, A	e 450,	Ф	æ	e 199	æ	2	e 2,	e 121	2219	Sequence 17, Appl	o. 522911	æ	O	e 50877,	e 35660,	e 21131,	e 25228,	Œ	e 6450,	e 417	nce 5558,	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	8
6	σ	6	6	σ	6	σ	σ	6	σ	σ	6	0	6	6	σ	σ	σ
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348	348	348	348	348	348	347	344	339	336	329	325	316	309	306	298	294	497
4	4	w	w	μ	_	4	4	4	w	4	ω	4	4	w	4	4	4
US-09-291-046-17	US-09-291-046-8	US-09-064-033-17	US-09-064-033-8	US-08-454-196-17	US-08-454-196-8	US-09-252-991A-31647	US-09-248-796A-16383	US-09-107-532A-5514	US-09-105-390-52	US-09-149-476-483	US-09-134-001C-3551	US-09-252-991A-25345	US-09-489-039A-8203	US-09-105-390-36	US-09-134-000C-5845	US-09-540-236-3779	US-09-252-814-25341
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	aprianhae
17, Appl	8, Appli	17. Appl	8, Appli	17, Appl	8, Appli	31647, A	16383, A	5514, Ap	52, Appl	483, App	3551, Ap	25345, A	8203, Ap	36, Appl	5845, Ap	3779, Ap	4, TECC?

# ALIGNMENTS

밁 Ś US-09-583-110-4172 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-513-999C-5558 RESULT 1 US-09-513-999C-5558 FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR PPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961 FILE REFERENCE: 59 US2.REG SEQ ID NO 5558 LENGTH: 51 GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y. GENERAL INFORMATION: Sequence 4172, Application US/09583110 Patent No. 6699703 Matches Query Match Best Local ( Sequence 5558, Application US/09513999C Patent No. 6783961 CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Pacent.pm APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics Local 25 EEKNVL 30 33 EEKNVL 38 Similarity 6; Conserv Conservative 100.0%; 14.6%; Score 6; Pred. No. 0 Mismatches DB 4; Length 51; 0; Indels 0; Gaps

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RESULT 4
US-09-513-999C-4616
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US-09-621-976-6450
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                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4616, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patent.pm
SEQ ID NO 6450
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Matches 6; Conserv
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LENGTH: 61
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ESTs and Encoded Huma:
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION UNMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                              LOCATION: -48..-1
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                FILE REFERENCE: 59.US2.REG
                                                                                FEATURE:
NAME/KEY: SIGNAL
                                                                                                               ORGANISM: Homo sapiens
NAME/KEY: UNSURE
                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ERKEEK 56
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Duclert, A.
--dano, J.Y.
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                                                 score 3.8
                              seq NSLLLLLCLYIYP/HS
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Candida albicans
US-09-248-796A-25228
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Sequence 21131, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21131
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25228
LENGTH: 88
LENGTH: 88
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATEMIN Ver. 2.0
SEQ ID NO 50877
LENGTH: 99
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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SEQ ID NO 35660
LENGTH: 99
TYPE: PRT
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RESULT 9 US-09-270-767-38390

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RESULT 11
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US-09-270-767-53607
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                                                                                                            PATENT NO. 5229115

APPLICANT: LYNCH, DAVID H.

TITLE OF INVENTION: ADOPTIVE IMMUNOT

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/559,001

FILING DATE: 26-JUL-1990
                                                                                               SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER: OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 53607
LENGTH: 127
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: file Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 38390

LENGTH: 127
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Patent No. 6703491
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US-09-708-200-17
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GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND
                                                       Sequence 1214, Application US/09710279 Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 22195
LENGTH: 135
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Patent No. 6576468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22195, Application US/09248796A
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CURRENT APPLICATION NUMBER: US/09/708,200
CURRENT FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nicolaides, Nicholas C
APPLICANT: Grasso, Luigi
APPLICANT: Sass, Philip M
TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
TITLE OF INVENTION: HYPERMUTABLE CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 133
                                                                                                                                                              55
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                                                                                                                                                                                                                                             14.6%;
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                                                                                                                                                                                                                                 0
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CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 1214
                                                                                                                    COMPUTER: Apple Macintosh
ODERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.:
SOFTWARE: Microsoft Word, Version 5.:
SOFTWARE: Microsoft Word, Version 5.:
CURRENT Application NUMBER: US/08/446,908
FILING DATE: 22-MAY-1995
CLASSIFICATION NUMBER: US 08/231,205
FILING DATE: 21-APR-1994
APPLICATION NUMBER: US 07/957,649
FILING DATE: 21-APR-1994
APPLICATION NUMBER: US 07/957,649
FILING DATE: 06-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-0CT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/113,566
APPLICATION NUMBER: US 07/113,566
APPLICATION NUMBER: US 07/113,566
APPLICATION DATE: 26-0CT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Namen, Antl
APPLICANT: Goodwin, Re
APPLICANT: Lupton, Ste
APPLICANT: Mochizuki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 147
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les 6; Conserv
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51 University Street
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Lupton, Stephen D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Diane Y.
Interleukin-7 and Antibodies Reactive
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100.0%; Pred. No.
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TELEFAX: (206) 233-0644;

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acids
TYPE: amino acids
MOLECULE TYPE: protein
US-08-446-908-2

Query Match
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy
32 KEKNV 37
| Db
119 KEEKNV 124

Search completed: February 1, 2005, 15:35:42
Job time: 18.5556 secs
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Minimum DB seq length: 21
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
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247.799 Million cell updates/sec
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                                                          Published Applications AA:*

1: /cgn2 6/ptodats/1/pubpas/PCT

2: /cgn2 6/ptodats/1/pubpas/PCT
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/ Cgn12 6/ptodata/1/pubpaa/US08 NEW PUB-COMB.pep: *
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/ Cgn12 6/ptodata/1/pubpaa/US09B PUB-COMB.pep: *
/ Cgn12 6/ptodata/1/pubpaa/US09A NEW PUB-Dep: *
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cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 2 2 2 3 3 3 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6	Regult
2 2 2 2 3 3 4 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Score
17.1 17.1 17.1 17.1 17.1 17.1 17.1 17.1	Query Match
1149 61 75 93 94 119 1186 232 232 319	% Query Match Length DB
115555555555555555555555555555555555555	8
US-10-128-558-167 US-10-767-701-52614 US-10-424-599-224449 US-10-424-599-157348 US-10-424-599-198515 US-10-424-599-271135 US-10-424-599-2713405 US-10-424-599-279781 US-10-424-599-279781 US-10-424-599-279781 US-10-424-599-157334 US-10-424-599-157334 US-10-424-599-157334 US-10-424-599-157334 US-10-424-599-232288	ID
Sequence 167, App Sequence 52614, A Sequence 224449, Sequence 157348, Sequence 198515, Sequence 271135, Sequence 283405, Sequence 279781, Sequence 279781, Sequence 157334, Sequence 157334, Sequence 232288,	Description

4 4 4 0	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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14.6 14.6	14.6	٠	14.6	٠	٠	٠	•	14.6	٠	•		•	14.6	14.6	•					14.6	•					17.1		•	17.1	17.1
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9	17	15	14	9	17	16	15	17	15	13	17	15	15	17	17	15	9	14	9	16	9	9	16	16	15	15	16	14	15	17
599-18751 )0-1880	US-10-425-115-264469	-10-424-599-23849	348-	92-4	-10-425-115-264	-10-437-963-16942	-10-424-599-218	-10-425-115-33528	-10-282-122A-48	-10-002-344A-23	-10-425-115-35819	-10-424-599-1	-424-599-25416	-10-425-115-2	10-425-115-25	-242-515-	77-106	-371-634-2	-19	-10-767-703	09-864-761-	09-864-761-	-10-437-963	-10-437-963	-10-389-566	-10-389-566-8	-10-437-963-1096	-10-369-493-2	0-425-114-6293	US-10-425-115-323502
Sequence 187518, Sequence 1880, Ap		Sequence 238496,	Sequence 49, Appl	Sequence 49, Appl	Sequence 264251,	e 16	æ	O	e 48051,	e 231, Ap	Sequence 358196,	Ф	O		253833	e 1063	1063,	e 25,		Œ			e 15206	e 10962	Ø	e 822,	e 1096	e 20250	e 629	Sequence 323502,

# ALIGNMENTS

RESULT 1
US-10-128-558-167
Sequence 167, Application US/10128558
Publication No. US20040219521A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Gezhi
APPLICANT: Weng, Gezhi
APPLICANT: Byle, Bryan J
APPLICANT: Drmanac, Radoje T
ITITLE OF INVENTION: Novel Nucleic Acids and
TITIE OF INVENTION: Novel Nucleic Acids and
TITIE OF INVENTION: Novel Nucleic Acids and
TITIE OF INVENTION: Novel Nucleic Acids and
TITIE OF INVENTION: Novel Nucleic Acids and
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RESULT 3
US-10-424-599-224449
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                                                     ) OTHER INFORMATION: Clone ID: PAT_MRT3847_44706C.1.pep
US-10-424-599-224449
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Best Local Similarity
'``ches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: US-10-767-701-52614
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US-10-767-701-52614
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                                                                                                                                                      APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 224449
Query Match
Best Local Similarity
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Best Local Similarity
Matches 20; Conserv
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LENGTH: 61
TYPE: PRT
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SOFTWARE: pt FL genes Version
SEQ ID NO 167
LENGTH: 1149
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
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APPLICANT:
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                         FEATURE:
                                                                                                  ORGANISM: Glycine max
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                                                                                                                                           LENGTH: 75
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Conservative
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 17.1%;
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Pred. No.
 Score 7;
Pred. No.
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 DB 15; Length 75; . 24;
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US-10-424-599-198515
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                                                                   Best Loc
Matches
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 198515
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 157348
LENGTH: 79
TYPE: PRT
ORGANISM: Glycine max
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Matches 7; Conserv
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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ORGANISM: Glycine
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NAME/KEY: unsure
LOCATION: (1)..(79)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: Clone ID: PAT_MRT3847_113105C.1.pep
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PERKEEK 70
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o. 25;
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
TYPE: pom
RESULT 8
US-10-767-701-53909
; Sequence 53909, Application US/10767701
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US-10-424-599-271135
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LENGTH: 119
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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LOCATION: (1)..(119)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
FEATURE:
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nes 7; Conserv
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100.0%; Pred. No. 31;
ative 0; Mismatches
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US-10-424-599-157336; Application US/10424599; Sequence 157336; Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_94664C.1.pep
US-10-424-599-279781
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT ELING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 279781
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Best Local
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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LOCATION: (1).. (186)
OTHER INFORMATION: unsure at all Xaa locations
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TYPE: PRT
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les 7; Conserv
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Conservative
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APPLICANT:

Kovalic David Zhou Yihua

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RESULT 12
US-10-282-122A-52352
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Best Local Similarity
Matches 7; Conserva
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APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 157334

LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                   Sequence 52352, Application US/10282122A Publication No. US20040029129A1
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 157336
LENGTH: 232
                                                                                                                     APPLICANT:
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                                                                 APPLICANT
                                                                                                      APPLICANT:
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max FEATURE:
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ORGANISM: Glycine max
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NUMBRITION: Identification
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                                                                                                                                   Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                       Zamudio, Carlo
Malone, Cheryl
                                                                                 Carr,
                                                                                                  Trawick, John
                                                                                                                                                                        Haselbeck, Robert
                                                          Carr, Grant
Yamamoto, Robert
                                        forsyth, R.
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                                                                                                                  Daniel
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100.0%;
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US-10-424-599-232288
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SEQ ID NO 52352
LENGTH: 308
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SEQ ID NO 232288
LENGTH: 319
                                                                                                                  Query Match
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Best Local
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-23
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                                                                          Similarity 7; Conserv
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Pred. No.
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o. 82;
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APPLICANT: Lii, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Xovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62939
LENGTH: 332
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: LIB3069-044-D11_FLI.pep
US-10-425-114-62939
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
CURRENT FILING DATE: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 32502
LENGTH: 324
TYPE: PRT
ORGANISM: Zea mays
PEATURE:
ORGANISM: Zea mays
PEATURE:
OTHER INFORMATION: Clone ID: MRT4577_58103C:1.pep
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Sequence 62939, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Publication No. US20040214272A1
GENERAL INFORMATION:
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B70181
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-330 <MUR>

A; Reference number: Z21576 A; Accession: T35360

R; Murphy, L.; Harris, D.; James, K.I submitted to the EMBL Data Library,

C; Accession: T35360

RESULT 1

probable membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

K.D.; Parkhill, J.; Barrell, B.G.; Rajandream,

M.A.

A; Cross-references: UNIPROT:Q9XALO; A; Experimental source: strain A3(2)

EMBL:AL079348; PIDN:CAB45459.1; GSPDB:GN00070; SCOED

## ALIGNMENTS

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A; Rotes preliminary
A; Status: preliminary
A; Rotecule type: DNA
A; Residues: 1-435 <ARN>
A; Cross - references: UNIPROT: Q9WXV3;
A; Cross - references: UNIPROT: Q9WXV3;
A; Cross - references: UNIPROT: Q9WXV3;
A; Cross - references: Strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein - Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (strain MSB8) (;Speciles: Thermotoga maritima (st
A;Gene: TM0098
C;Superfamily: GTI
F;165-290/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999
A;Title: Byidence for lateral gene transfer between Archaea and Bacteria from genome seq.
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GAENPDP 115
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GTP-binding protein obg; translation elongation factor Tu homology in: translation elongation factor Tu homology <ETU>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                GB:AE001696; GB:AE000512;
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Query Match Best Local Similarity

17.1%; 100.0%;

Score 7; 1 Pred. No.

DB 2;

Length 435;

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RESULT
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano.; H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F19G10.17 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86362
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                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A86141; MUID:21016719;
A;Accession: F86362
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C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
F;300-469/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9SMP5; EMBL:AL133315
A;Experimental source: cultivar Columbia; BAC clone T8P19
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cati
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23008
A;Accession: T46196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-506 < CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome P450-like protein - Arabidopsis thalia
N;Alternate names: protein T8P19.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                    ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                   Residues:
                                                                                                                                                                            Query Match
Best Local
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Best Local
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                                                                                                                                                     Conservative
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100.0%; Pr
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100.0%; Pred. No.
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o. 17;
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<u>,</u>

Mismatches

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0

Gaps

<u>.</u>

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Filo78-1158/Domain: Fibronectin type III repeat homology <3F5>
Filo78-1158/Domain: Fibronectin type III repeat homology <3F5>
Fil248-131/Domain: Fibronectin type III repeat homology <3F6>
Fil248-131/Domain: Fibronectin type III repeat homology <3F6>
Fil248-131/Domain: Fibronectin type III repeat homology <3F6>
Fil323-1403/Domain: Fibronectin type III repeat homology <3F9>
Fil510-1590/Domain: Fibronectin type III repeat homology <3F10>
Fil618-1676/Domain: Fibronectin type III repeat homology <3F10>
Fil618-1676/Domain: Fibronectin type III repeat homology #status atype Fil678-1749/Domain: Fibronectin type III repeat homology <3F13>
Fil618-169/Domain: Fibronectin type III repeat homology <3F13>
Fil618-169/Domain: Fibronectin type III repeat homology <3F14>
Fil618-169/Domain: Fibronectin type III repeat homology <3F15>
Fil618-169/Domain: Fibronectin type III repeat homology <3F16>
Fil618-169/Domain: Fibronectin type III repeat homology <3F18>
Fil618-2045/Domain: Fibronectin type III repeat homology <3F18>
Fil618-2045/Domain: Fibronectin type III repeat homology <3F19>
Fil618-2046/Domain: Fibronectin type III repeat homology <3F19>
Fil618-2046/Domain: Fibronectin type III repeat homology <3F20>
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Fil61
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A;Residues: 2748-3199,'V',3201-3298,'E',3299-3314,'G',3316-3566 <MOR>
A;Residues: 2748-3199,'V',3201-3298,'E',3299-3314,'G',3316-3566 <MOR>
A;Cross-references: GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:g183070
R;Matsumocto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.
Genomics 12, 485-491, 1992
A;Title: Cluster of fibronectin type III repeats found in the human major histocompatible.
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(Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-
C;Accession: A40701; A33725; C42175
R;Bristow, J.; Tee, M.K.; Gitelman, S.E.;
J. Cell Biol. 122, 265-278, 1993
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A; Residues: 1849-1936 < MAT>
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A;Molecule type: DNA
A;Residues: 1-3566 <BRI>
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A;Map position: 6p21.3-6p21.3
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A;Accession: A40701
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;435-461/Domain: EGF homology <EGF>
;748-828/Domain: fibronectin type III repeat homology <3F1>
;829-856/Domain: fibronectin type III repeat homology #stati
;873-953/Domain: fibronectin type III repeat homology <3F3>
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hypothetical protein CP0881 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81526 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2403
R;Horii, A.; Han, H.J.; Sasaki, S.; Shimada, M.; Nakamura, Y.
Biochem. Biophys. Res. Commun. 204, 1257-1264, 1994
A;Title: Cloning, characterization and chromosomal assignment of the human
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: C70306
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C;Specias: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: C70306
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A; Residues: 1-77 < AQF>
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A;Experimental source: strain AR39;
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A; Residues: 1-45 < REA>
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                                                                    A;Cross-references: UNIPROT:P49446
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Sc
submitted to the EMBL Data Library, June 195
A;Description: Assessment of the expression
A;Reference number: S40280
                                                                                                                                                                                                                                                         C;Accession: B61180; S40283
R;Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 191.
A;Title: Identification of novel protein tyrosine phosphatases of hematopoietic A;Reference number: A61180; MUID:92032882; PMID:1932742
A;Accession: B61180
                                                                                                                                                                                                                                                                                                                                                                                                protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon - mouse (N;Alternate names: protein-tyrosine-phosphatase PTPTY8
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
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  A;Accession: S40283
A;Molecule type: mRNA
A;Residues: 1-30,'T',32-109 <HEN>
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A; Residues: 1-109 < YIA>
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Schepens, J.; Wieringa,

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(fragment)

cells

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levels of

murine protein-tyrosine phosphatas

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A;Cross-references: UNIPROT:O51595; GB:AE001166; GB:AE000783; NID:g2688571; PIDN:AAC6699 A;Experimental source: strain B31 C;Superfamily: yajC protein
                                                                                                                                                                                                                                                                                Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, A;Fitle: Genomic sequence of a Lyme disease spirochaete, A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70181
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B70181
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A;Map position: 7q11.23-7q22
C;Keywords: DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: JC2398; MUID:95071462; PMID:7980603
A;Accession: JC2403
                                                                                                                                                                                                                                                                                                                                                                R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein BB0651 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-98 <HOR>
A;Cross-references: UNIPROT:Q16590; DDBJ:D38440; NID:g600595; PIDN:BAA07475.1; PID:d1008
                                                                                                                                                                                                                          A;Residues: 1-105 <KLE>
                                                                                                                                                                                                                                          A; Molecule type: DNA
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43
                                     31 RKEEKN 36
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RKEEKN 48
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Pred. No.
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RESULT
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A;Note: the source is designated as Spalax ehrenbergi
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic ribonuclease (EC 3.1.27.5) - Ehrenberg's mole-rat C;Species: Spalax leucodon ehrenberg's (Ehrenberg's mole-rat) C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Ju: C;Date: 28-Feb-3990 #sequence_revision 28-Feb-1990 #text_change 09-Ju: C;Accession: 804503; A32505 R;Schueller, C.; Neuteboom, B.; Wuebbels, G.H.; Beintema, J.J.; Nevo, Biol. Chem. Hoppe-Seyler 370, 583-589, 1989
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                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The amino-acid sequence of pancreatic ribonuclease A;Reference number: S04503; MUID:89374807; PMID:2673297 A;Accession: S04503
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C;Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antig
C;Keywords: phosphoric monoester hydrolase; receptor; transmembrane protein; tyrosine-sp
F;1-109/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>
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A;Experimental source: strain A3(2)
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A;Accession: T34582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, January 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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T34582
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                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                    ;Keywords: glycoprotein; hydrolase
;12,42,120/Active site: His, Lys, His #stat
;27-85,41-96,59-111,66-73/Disulfide bonds:
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Best Local
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6; Conserv
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100.0%; Pred. No. 56
tive 0; Mismatches
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100.0%; Pred. No. 52;
tive 0; Mismatches
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100.0%; Pred. No.
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(strain C58,
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A;Reference number: A70300; MUID:98196666; PN A;Accession: A70411
A;Status: preliminary; nucleic acid sequence A;Molecule type: DNA
                                                                                                                                                                              C;Species: Aquifex acolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
                                                                                                        Nature 392, 353-358, 1998
                                                                                                                                                C;Accession: A70411
R;Deckert, G.; Warr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-141 < KUR>
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A; Map position:
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C;Date: 11-Jan-2002 #text_change 09-Jul-2004
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2997
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Cross-references: UNIPROT:Q8U9Z3; GB:AE008689;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: E98286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AGR L_2491 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Accession: E98286
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Q9gm44 macaca fasc
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	RESULT QBN7L7 ID 7C AC QQ DT 00 DT 00 DT 00 CC	
SEQUENCE FROM N.A. TISSUE=Uterus; PhibMed=14702039; Ota T., Suzuki Y. Wakamatsu A., Hayy Sekine M., Obayasi Yamamoto J., Saito Muzakami K., Yasu Sudo H., Hosoiri Takahashi M., Kan Abe K., Kamihara I Ninomiya K., Takil Tanai H., Kimata I; Ono Y., Takiguchi Kanehori K., Takil Tanai H., Kimata Y. Musashino K., Yuul Yoshikawa Y., Maty Musashino K., Yuul Yoshikawa Y., Momiyat Moriya S., Komai J. Musashino K., Yuul Yoshikawa Y., Momiyat Musashino K., Yuul Yoshikawa Y., Momiyat Musashino K., Yuul Yoshikawa Y., Momiyat Musashino K., Yuul Yoshikawa Y., Maki Togaya S., Momiyat Musashino K., Wayak Moriya S., Momiyat Moriya S., Momiyat Moriya S., Momiyat Moriya S., Momiyat Ono T., Yamazaki M., Wataa Fujimori Y., Komiyat Ono T., Yamazaki M., Wataa Fujimori Y., Wayas Mataumura K., Nayas Nakai K., Yada T. "Complete sequenc: CDNAB: " Nat. Genet. 36:40- EMBL; AK098212; BJ InterPro; IPR0089.	1 8N71 8N71 1-00 11-00 ppo pomo puka:	S S S S S S S S S S S S S S S S S S S
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Query Match 100.0%; Score 41; DB 2; Length 897; Best Local Similarity 100.0%; Pred. No. 5.1e-34; Matches 41; Conservative 0; Mismatches 0; Indels

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FLJ10359 protein (Fragment).
Name=FLJ10359;
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REPEAT
     MEDLINE=22388257; PubMed=12477932;
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Mammalia; Eutheria;
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InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
01-0CT-2004 (Rel. 45, Last ann
Protein BAP28 (QnpA-17571) (Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GM44;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MACFA
                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osada N., Hida M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=BAP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the BAP28 family.
SIMILARITY: Contains 1 HEAT repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MACFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKLLCKNFGAENPDPFVPVLSTAVKLIAPERKEEKNVLGSA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKLLCKNFGAENPDPFVPVLSTAVKLIAPERKEEKNVLGSA
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958 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kusuda J., Tanuma R., Iseki
S., Hashimoto K.;
                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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annotation update)
(Fragment).
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N; 3DBD95C3623CFB31 CRC64;
                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krozwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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RA Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Hopkins R.F., Jordan R., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Walki T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Nones S.J., Marra M.A.;
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Best Local
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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NON_TER 1
SEQUENCE 1106 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymph;
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41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125359 MW;
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27,
27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; I
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RX PubMeda14702039; DOI-10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Yamaroto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Yamaroto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Yamaratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Gunura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Rusano J., Kanehori K., Takahashi T., Yamashita H., Murakawa K.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Yoshikawa Y., Matsunawa H., Ichihara R., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Hishigaki H., Watanabe T., Sujiyama A., Sasaki N., Saveb H.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sujiyama A., Takemoto M., Sanoši S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Sanoh T., Matanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
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Mammalia; Eutheria; Primates;
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BC065205; AAH65205
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, 04-JAN-2001.
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Catarrhini; Hominidae;
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Nakai K.,
         IJkel W.F.J., van Strien E.A., Heldens J.G.M., Goldbach R.W., Vlak J.M.;
Goldbach R.W., Vlak J.M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ (EMBL, AF169823; AAF33588.1; -...
InterPro; IPR009313; Baculo 11 kDa.
Pfam; PP06143; Baculo 11 kDa; I.
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                                                                                                        "Sequence and organization of the nucleopolyhedrovirus genome.";
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20036646; PubMed=10567663;
IJkel W.F., van Strien E.A., Helde
Goldbach R.W., Vlak J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AX067150; CAC26776.1; -. EMBL; AL136105; CAC15948.1; -.
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                                                                                                                                                                                               Viruses; dsDNA viruses, Nucleopolyhedrovirus.
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AK001221; BAA91564.1;
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an email to license@isb-sib.ch).
                                                                                               Virol.
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ada T., Nakamura Y., Ohara O.,
equencing and characterization
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hara O., Isogai T., Sugano S.;
rization of 21,243 full-length hun
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                                                                                                                     spodoptera
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B stownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B stownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hopkins R.F., Johnson J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Tones G. T. Marra M.A.
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Hypothetical protein.
Kenopus laevis (African clawed frog).
Kenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                 Klein S., Strausberg R.;
Submitted (JUN-2004) to the
EMBL; BC075194; AAH75194.1;
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SEQUENCE 209 AA; 2
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Klein S.L., Strausberg R.L., Wagner L.,
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Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
                                                                                                                                                                                                                                                                                             ATP-binding; Complete proteome; Isoprene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100; Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H. Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
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PRINTS; PR00958; HOMSERKINASE.
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InterPro; IPR004424;
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Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Clostridium tetani, the causative agent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Massachusetts / E88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
1-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                     9
                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By similarity).

CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the GHMP kinase family. IspE subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Nonmevalonate terpenoid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLOTE
                                                                                                              204
                                                                                                                                        1 LKLLCKN 7
                                                                                                                                                                 Similarity 7; Conserv
                                                                                                              LKLLCKN
                                                                                                                                                                                                                           133
280 AA;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                       91
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                         101 A
8 B
133 B
133 B
                                                                                                                                                                                                                                                                                                                                                        IspE.
                                                                                                                                                                                                                                                                                                                                                               Homoser_kin.
                                                                                                                                                                                                                                                                                                                                                                                  GHMP_kinase.
                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                17.1%;
                                                                                                                                                                    0;
                                                                                                                                                                                 Score 7;
Pred. No
                                                                                                                                                                                                                                     ATP (Potential).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                           B132AC792B8CDD7F CRC64;
                                                                                                                                                                   mismatches
                                                                                                                                                                         DB
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280
                                                                                                                                                                                                                                                                                                                                                                                                                                                   noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                               1;
                                                                                                                                                                                               Length 280;
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kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fourth
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Q72JR4; 05-JUL-2004 05-JUL-2004

(TrEMBLrel.

27,

Created) Last seq

sequence update)

Q72JR4

PRELIMINARY;

PRT;

284

A

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RESULT 11
Q9XAL0
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Best Local
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Best Local
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Q9XAL0
Q9XAL0;
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nat. Biotechnol. 22:547-553(2004).
EMBL; AE017303; AASB1052.1; -
INTERPRO; IPR003838; DUF214.
Pfam; PF02687; FteX; 1.
Cell division; Complete proteome.
SEQUENCE 284 AA; 31042 MW; 36FAC9F453CA7FAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermophilus.";
Nat. Biotechnol. 22:547-553(2004).
EMBL; AE017303; AAS81052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T.,
Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R.,
Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
"The genome sequence of the extreme thermophile Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-2004 (TrEMBLrel. 27,
14-APR-2004 (TrEMBLrel. 27,
11-MAY-2004 (TrEMBLrel. 27,
Cell division protein ftsX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=15064768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS81052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS81052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15064768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=262724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Deinococcus-Thermus; Deinococci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=ftsX; OrderedLocusNames=TTC0704;
Thermus thermophilus (strain HB27 / A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         division.
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                              PFVPVLS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STAdadd
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   (TrEMBLrel. 12,
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                                                                           PRELIMINARY;
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100.0%; Pr/
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Last annotation update)
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inococci; Thermales; Thermaceae;
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5. 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 284;
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Best Local
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STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.B., Quall M.A., Kieser H.,

Thomson N.B., James R.D., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,

Rubbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Rabbinowitsch E., Sanders B., Squares R., Squares S., Taylor K.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
                                                                                                                STRAIN=CZA / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
FitzHugh M., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Metcalf W.W., Birren B.;
"The Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Company of Machanian Compa
Genome Res. 12:532-542(2002).
EMBL; AE010731; AAM04143.1; -
GO; GO:0003677; F:DNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 417:141-147(2002).
EMBL; AL939117; CAB45459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces "Controlor A1(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative membrane protein. OrderedLocusNames=SCO3592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Last 01-JUN-2003 (TrEMBLrel. 24, Last
                                                                         "The genome of Methanosarcina acetivorans and physiological diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=MA0703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005135; Exo_endo_phos
Pfam; PF03372; Exo_endo_phos; 1.
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Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2214;
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100.0%;
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Last
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Wat Klausner R.D., Collins F.S., Wagner L., Schmenen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M.J. Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M.J., Uddin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Robest S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pihey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzwinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

Ban Janes G. T. Marya M. A.
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Belongs to the PP2C family.
EMBL; BC072312; AAH72312.1; -
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C-1ike.
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SWART; SW0481; POLITIAC; 1.
Complete proteome; Hypothetical protein.
Complete proteome; Hypothetical protein.
SEQUENCE 334 AA; 38654 MW; 1BCACBAB4752B316 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Klein S.L., Strausberg
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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                                                                                                                                                                                    TISSUE=Ovary;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22341132;
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GO; GO:0006260; P:DNA replication; IEA.
InterPro, IPR003141; Pesterase_PHP_N.
Pfam; PF02231; PHP_N; 1.
                                                                                                                                                                                                                                                                                              nitiative
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                                                                                                                                                                                                                                                                                                                                                                     PubMed=12454917;
sberg R.L., Wagne
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27,
27,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                        Wagner L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                     Xenopus research: The NIH Xenopus
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A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length human
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RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Toshiyuki S., Casrainci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., William R.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Ra Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Xan Karywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Arnes G. J. Mayers M.M., Schein J.E.,
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SMART; SM00331; PP2CG; 1.
SMART; SM00331; PP2C SIG; 1
PROSITE; PS01032; PP2C; 1.
Hydrolase; Magnesium.
SEQUENCE 373 AA; 41536 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2004
01-JUN-2004
01-JUN-2004
                                                                                               EMBL;
                                                                                                                                                                                              "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                 Klein
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
Xenopodinae; Xenopus; Xenopus
                                                                                                                                                    TISSUE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richardson P.;
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Xenopus laevis (African clawed frog).
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Klein S.L., Strausberg R.L., Wagne
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                                                             al protein.
373 AA; 4
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373 AA; 41536 MW;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                             41536 MW;
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100.0%;
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                                                             58713D1A52099BB7 CRC64;
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Matches 7; Conserv
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R GO; GO:000525; F:GTP binding; IEA.

R InterPro; IPR006074; GTP1/OBG dom.

R InterPro; IPR006073; GTP1_OBG.

R InterPro; IPR006169; GTP1_OBG sub.

R InterPro; IPR006169; GTP1_OBG; 1.

R Pfam; PF01018; GTP1_OBG; 1.

R PRINTS; RR00326; GTP1_OBG; 1.

R PRINTS; RR00326; GTP1_OBG; 1.

R PROSITE; PS00905; GTP1_OBG; 1.

Complete proteome; Hypothetical protein.

SEQUENCE 435 AA; 48595 MW; 45A496703A4F74D2 CRC64;
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PRELIMINARY;
O9WXV3;
O1-NOV-1999 (TrEMBLrel. 12, C:
O1-NOV-1999 (TrEMBLrel. 12, L:
O1-UN-2003 (TrEMBLrel. 24, L:
Hypothetical protein.
OrderedLocusNames=TM0098;
                                                                                                                                                                                                                                    HSSP; P20964; 1LNZ.
TIGR; TM0098; -.
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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The present in length cDNAs da (a) an oligo-d complementary nucleotide seg oligonuc of an oligonuc complementary	Primer sets for syn length cDNAs define diagnosis of the ab cDNAs.	Ota T, Isogai T, Ishii S, Sugiyama WPI; 2001-318749/34	29-JUL-1999; 99J 27-AUG-1999; 99J 11-JAN-2000; 2000J 02-MAY-2000; 2000J 09-JUN-2000; 2000J	07-FEB-2001. CX 28-JUL-2000; 2000EP-	PN EP1074617-A2.	OS Homo sapiens.	CX Human; primer; detec	DE Human protein sequence	OT 26-JUN-2001 (first	AAB92729;	SULT 1 B92729		26 6 14 6
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bes primer sets for syspecification. Where a no ligonucleotide compilynucleotide which compin the specification the specification, least 15 nucleotides; sing a sequence completynucleotide which compine the specification that it is nucleotides in the specification that it is nucleotide which compine the specific speci	polynucleotides, pa specification, and f of the proteins end	nikawa T, Hayashi K, Saito Wakamatsu A, Nagai K, Otsu					agnosis; antisense the	ID NO:11159.		;	340 33	ALIGNMENTS	AAOO4449  AAGO0262  AAU18927  AAU96713  ABG21112  AAM96713  ABG21112  AAM06778  AAM06778  AAM06775  AAOO3971  AAOO3971  AAOO3971  AAOO3991  AAU66665  AAU76666666666666666666666666666666666
nthesising 5602 full- primer set comprises: lementary to the prises one of the 5602 where the or (b) a combination mentary to the prises a 5'-end	cularly the dete d by the	OK, Yamamoto J;					rapy; gene therapy.						Aao04449 Human pol Aag00262 Human sec Aau18927 Novel pro Aau22275 Human car Aam96713 Human rep Abg21112 Novel hum Ade46243 Human imm Aam06778 Human foe Aao08667 Human pol Aao09971 Human pol Aao09971 Human pol Aao1956259 Human non Aao11546 Human pol Aao15665699 Human pol Aao06065 Human pol Aao06065 Human pol Aao16066 Human pol Aao16066 Human pol Aao89592 Human pol Aao89592 Human imm Aam89592 Human imm Aam89592 Human imm Aam89592 Human sec

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Matches 41
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-0376045P.
24-APR-2002; 2002US-0376045P.
New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tin which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                         Ghosh
Ma Y,
                                                                                                                                                     WPI; 2003-569235/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods AH03166 to AH13628 and AH13633 to AH18742 represent human cDNA sequences; AH92446 to AH95893 represent human amino acid sequences; and AHH3629 to AHH3632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel protein
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                                                                                                                                                                                                   T, Asundi V, Goodrich RW,
M, Xue AJ, Wehrman T, Wen
Wang D, Chen R, Xu C, Bc
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Pred. No. 5.5
0; Mismatches
                                                                                                                                                                                                      RW, Ren F, Zhang J, Zhao
Weng G, Zhou P, Drmanac
Boyle BJ;
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The invention proteins. The

comprises the amino acid and DNA and protein sequences of ID NO 1078; 1177pp; English.

coding sequences of novel the invention are useful

a8:

Claim 20;

SEQ

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RESULT 3
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ID AAW5
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                                                                              The sequence is that of a protein which can be used in the preparation of CC the recombinant breast cancer antigen, BRCA1, binding proteins BARD1, CC B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a CC BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid sequence, specifically CC a wild type BARD1 composition for the detection or purification of BRCA1, CC useful to identify a patient having, or at risk of developing cancer. CC BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, CC BE14, BE31 or BE445 can used in the identification of barD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to antibody can be used to identify a patient having or at risk of
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03-APR-1997;
04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer.
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N-PSDB; AAV24135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 287-288; 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowcock AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BARD1; ring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; BRCA1; breast cancer; risk; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baer R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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97US-0042611P.
97US-0042985P.
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100.0%; Pred. No.
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Query Match Best Local

Similarity

48.8%; Score 20; 100.0%; Pred. No.

3.9e-13; DB 2;

Length 515;

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RESULT 4
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XXX AAB8
XXX AAB8
XXX Prot
XXX Prot
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Matches 20; Conserv
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                                                                                                                                                                              The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3 and 5 ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polypeptides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first CDNA sequence of the BAP28 gene consisting of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barry C,
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                                                                                                            Sequence 2144 AA;
                                                                                                                                                                encoded by a :
exons 1 to 45
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18-JAN-2000; 2000US-0176880P.
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48.8%; Score 20; DB 4; Lidarity 100.0%; Pred. No. 1.3e-12; Conservative 0; Mismatches 0;
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2017
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                                                 Length 2144;
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Indels

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Gaps

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RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, soing the recombinant expression regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 411
                                               Antisense; prokaryotic essential gene; cell proliferation;
                                                                                                       Protein
                                                                                                                                                             19-JUN-2003
                                                                                                                                                                                                                  ABU42163;
                                                                                                                                                                                                                                                                  ABU42163 standard; protein; 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7912; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACH94946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant
Klebsiella p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella pneumoniae polypeptide seqid
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                                                                                                       encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression vector;
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                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                    Prokaryotic essential gene #27690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.5%; Score 8; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 411;
                                                  drug design.
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WO200277183-A2

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the 6213 antisense squences given in the specification where expression (C (1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are: (2) of the nucleic acid inhibits promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense c nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide of specifically binding c the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of crequired for proliferation, or that has an activity against a biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a culture compound that inhibits proliferation of an organism acts; (1) identifying a natibiotic; (10) profiling a compound to which each of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational correquired for proliferation to isolate candidate molecules for rational correquired for proliferation in cells other than S. aureus, S. typhimurium, C. Experiment did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the target prokaryotic essential genes. Note: The sequence data for this can be attended to proliferation format of the printed specification, but was obtained con an electronic format directly from WIPO at
                                                                                             Query Match
Best Local (
                                                                           Matches
                                                                                                                                                      Sequence 443
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-029926/02.
N-PSDB; ACA46033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising any one of
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67
                                   34 LTAFFLEA 41
                                                                        l Similarity
8; Conserv
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 70087; 1766pp; English.
                                                                      19.5%; Score 8; DB larity 100.0%; Pred. No. 3. Conservative 0; Mismatches
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Carr G
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Yamamoto R,
                                                                                         DB 6;
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Forsyth RA,
                                                                                                            Length 443;
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Xu HH;
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ADF06196 standard; protein; 457 AA.

ABM69250 RESULT 7

ABM69250 standard; protein; 446 AA

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CC polypeptides encoded by the genes are used for detection/identification (CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that CC carry a gene-containing vector are used to select compounds that CC modulate, regulate, induce or inhibit expression of the genes in plants, CC animals or microorganisms other than P. luminescens and are able to alter CC response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for CC recombinant production of the proteins, particularly toxins and antibioters proteins, vectors containing the genes and Ab are also useful CC antibacterials useful as insecticides, bactericides and fungicides. The CC genes, proteins, vectors containing the genes and Ab are also useful CC therapeutically (to treat microbial infection by bacteria or fungi that CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as CC biopesticides. Other uses of the genes and the proteins are as virulence factors and foor identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of p. luminescens and related species; to study polymorphisms, for gene analysis and for detection, amplification of the genes. Antibodies (Ab) raised against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                       Local
103 LTAFFLEA 110
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                                                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                          446 AA;
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                                                                                                                                       Conservative
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                                                                                                                                                                Score 8; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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                                                                                                                                                                    DB 6;
                                                                                                                                                                                                     Length 446
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RESULT 9
ABU40177
ID ABU40
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymuclectides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial drugs or as blo-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
                             WO200277183-A2
                                                        Pseudomonas putida
                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                              Protein encoded by Prokaryotic essential gene #25704.
                                                                                                                                            19-JUN-2003
                                                                                                                                                                         ABU40177;
                                                                                                                                                                                                     ABU40177 standard; protein; 467
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new Proteus mirabilis polypeptides and polynucleotides. The invention also relates to antibodies against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breton GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteus mirabilis infection; bacterial infection; antibacterial;
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DB; ADF02024.
                                                                                                                                                                                                                                                                           110 LTAFFLEA 117
                                                                                                                                                                                                                                                                                                      34 LTAFFLEA 41
                                                                                                                                                                                                                                                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                 19.5%; Si
ilarity 100.0%; i
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03-OCT-2002

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ABO63337 standard; protein; 473 AA

29-JUL-2004 ABO63337;

(first entry)

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92

34 LTAFFLEA 41

Matches Query Match

8;

Conservative

19.5%; Score 8; DB 6; 100.0%; Pred. No. 3.5; .. •

Mismatches

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Gaps

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Length 467;

Best Local Similarity

Sequence

467

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pathway in which a proliferation required gene or its gene product lies (CC or a gene on which the test compound that inhibits proliferation of an CC organism acts; (9) manufacturing antibiotic; (10) profiling a cc compound's activity; (11) a culture comprising strains in which the gene cc compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent (12) determining the extent (13) identifying its present in a culture or collection of the strains is present in a culture or collection of the strains; or the antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to independent molecules for rational control of the proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation in cells other than S. aureus, S. typhimurium, control of the target prokaryotic essential genes. Note: The sequence data for this catent did not form part of the printed specification, but was obtained content in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                    (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies
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08-FEB-2002;
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06-SEP-2001;
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Forsyth
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Xu HH;
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RESULT 11
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Best Local S
Matches 8
     Breton GL
                                                                                                         09-APR-1999;
                                                                                                                                                           05-APR-2000;
                                                                                                                                                                                                             12-AUG-2003.
                                                                                                                                                                                                                                                                 US6605709-B1
                                                                                                                                                                                                                                                                                                                   Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                 Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial polypeptide #360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF04247;
                                                                                                                                                                                                                                                                                                                                                                           immunostimulant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                       (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF04247 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-895346/82.
N-PSDB; ACH96888.
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                                                    THERAPEUTICS CORP.
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RESULT 12
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                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
The invention relates to polynucleotides encoding
                                                                                Disclosure; SEQ ID NO 20403; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new Proteus mirabilis polypeptides and polypeptides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                           N-PSDB; ABD05228
                                                                                                                                                                                                                                                                                      WPI; 2003-615309/58.
                                                                                                                                                                                                                                                                                                                                               Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
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                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biocontrol agents for
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N-PSDB; ADF00075.
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98US-0094190P
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Pseudomonas aeruginosa polypeptides and the them. The sequences are useful in diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAGA-)
                                                                                                                                                                                                                         This invention describes a novel gene (AtMIDIB) encoding an extension-
activated calcium (Ca2+) permeable channel of higher plant, useful for
controlling gravity tropism in plants. The gene is useful as gravity
sensor in plant. Transgenic plants containing the gene have improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel AtMID1B gene derived from Arabidopsis thaliana encoding extension-
activated calcium permeable channel, useful for maintaining gravity
tropism in plant.
                                                                                                                              Sequence
                                                                                                                                                                                                 photosynthetic ability.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 2; 11pp; Japanese.
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                              Local
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DB; ADG36881.
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   Similarity 7; Conserv
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   17.1%; Score 7; DB ...
llarity 100.0%; Pred. No. 38
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                                                                                  complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a sequence complementary to a
coligonucleotide which comprises a 3'-end sequence, where the
polynucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
represent human amino acid sequences, and AAH13629 to AAH13632 represent
coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T,
Ishii (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8;
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNAs.
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                                                                 invention
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, Sugiyama T, Wakamats
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1 A, Nagai K
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C, Otsuki
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Query Match Best Local Matches

Similarity

17.1%;

Score 7; DB 4; Pred. No. 38; 0; Mismatches

DB . 4.

Length 417; Indels

Conservative

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RESULT 15
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                                                                                                                                                                                                                                           ANY49137-Y49152 are amino acid sequences that are fragments of choline combining proteins (CBP). The fragments of the protein are the alpha helix combining parts of the CBPs from Streptococcus pneumoniae. The polypoptides combine to contain the actual choline binding fragment. The polypoptides and the nucleotide sequences that encode them (AAZ31077-Z31092) are used in the invention, which relates to polypoptide truncates of a pneumococcal curface binding protein containing the highly conserved immunogenic alpha combines because the first polypoptide are used for preventing (immunising) or treating invasive bacterial (especially conserved). Infections, especially otitis media (caused by pneumococcal) infections, especially otitis media (caused by pneumoniae), sepsis, meningitis and lobar pneumonia infections. CC prevention (passive immunity) and treatment of S. pneumoniae infections. CC prevention (passive immunity) and treatment of S. pneumoniae infections. CC with an immature immune system, or patients with an on going pneumococcal confection against a range of pneumococcal serotypes and it produces an configuration against a range of pneumococcal serotypes and it produces an improved and enhanced effect in preventing bacterial infections.
                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                 Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 64-65; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New pneumococcal proteins useful as vaccines and for diagnosis of pneumococcal infections.
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15-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of choline-binding protein fragment #1.
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                                                                   Local Similarity 100.
mes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koenig S,
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100.0%; Pred. No. 39
htive 0; Mismatches
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KKEELTS 80

Search completed: February 1, 2005, 15:20:13 Job time : 70.7778 secs

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      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match Length DB
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154.882 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                              US-09-489-039A-7912
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US-09-543-681A-4532
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US-08-714-741-46
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US-08-714-741-41
US-09-513-99C-4343
US-09-513-99C-4343
US-09-513-99C-4343
US-09-513-976-767-81841
US-09-134-001C-5232
US-09-134-001C-5232
US-09-134-001C-3670
US-09-136-657-3
US-09-136-657-3
US-09-138-618-1
US-09-185-818-1
US-09-185-818-1
US-09-328-352-6245
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US-08-990-571-18
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Sequence 7912, Ap
Sequence 6481, Ap
Sequence 9854, Ap
Sequence 20403, A
Sequence 20403, A
Sequence 40, Appli
Sequence 40, Appli
Sequence 41, Appli
Sequence 41, Appli
Sequence 57043, Ap
Sequence 5794, Ap
Sequence 5794, Ap
Sequence 6, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
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Sequence 12987, A
Sequence 11, Appli
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ch	RESULT 2 US-09-543-681A-6481 ; Sequence 6481, Application US/09543681A ; Patent NO. 6605709 ; GENERAL INFORMATION; APPLICANT: GARY BRETON TITLE OF INVENTION: NUCLEIC ACID AND AL TITLE OF INVENTION: DIAGNOSTICS AND TELLE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543, CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,70 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 ; SEQ ID NO 6481 LENGTH: 457 TYPE: PRI ORGANIZM: Proteus mirabilis US-09-543-681A-6481	34 LTAFFLEA          46 LTAFFLEA	Similarit 8; Conse	SULT 1  -09-489-039A-7912  Sequence 7912, Application US/09489039A  Patent No. 6610836  GENERAL INFORMATION: APPLICANT: Gary Breton et. al  TITLE OF INVENTION: PUBLICATION OF INVENTION: PUBLICATION OF INVENTION: PUBLICATION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF INVENTION OF SEQ ID NO MADER: US 60/117,7  PRIOR FILING DATE: 1999-01-29  NUMBER OF SEQ ID NOS: 14342  SEQ ID NO 7912  LENGTH: 411  TYPE: PRT  ORGANISM: Klebsiella pneumoniae  -09-489-039A-7912		6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
19.5%:	Cation US/0: ITON NUCLEIC AC: DIAGNOSTIO 9.1002-001 (NUMBER: US.) 1199-04-09 UMBER: US 61 1199-04-09 SS: 8344 mirabilis	ŭ Ë	19.5%; 100.0%; ative	pplication US/09489039A upplication US/09489039A upplication et. al v Breton e		3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Score 8; DB 4;	MINO HERAI 681A		Score 8; DB 4 Pred. No. 0.3 0; Mismatches	ULT 1  O9-489-039A-7912  equence 7912, Application US/09489039A  atent No. 6610836  ENERAL INFORMATION: APPLICANT: GATY Breton et. al  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS J  FILE REFERENCE: 2709.2004001  FULL REFERENCE: 2709.2004001  FULL REFILIGATION NUMBER: US/09/489,039A  CURRENT APPLICATION NUMBER: US 60/117,747  PRIOR APPLICATION NUMBER: US 60/117,747  PRIOR FILING DATE: 1999-01-29  NUMBER OF SEQ ID NOS: 14342  ENGTH: 411  TYPE: PRT  ORGANISM: Klebsiella pneumoniae  O9-489-039A-7912	ALIGNMENTS	US-09-569-098A-18 US-08-945-258-28 US-08-990-571-28 US-08-990-571-28 US-09-528-784A-28 US-09-528-784A-46 US-08-990-571-46 US-08-990-571-46 US-08-9528-784A-46 US-09-528-784A-46 US-09-528-784A-23 US-08-91-23 US-08-91-23 US-08-923-142A-23 US-09-528-784A-23 US-08-9528-784A-23 US-08-9528-784A-23 US-08-9528-784A-23 US-08-9528-784A-23 US-08-9528-784A-23 US-09-528-784A-23 US-09-528-784A-23 US-09-528-784A-23 US-09-528-784A-23 US-09-528-784A-23 US-09-528-784A-23 US-09-528-784A-23 US-09-528-784A-23
; Length 457;	EQUENCES		; Length 411; 8; 0; Indels	SEQUENCES		
-•	RELATING TO P		0; Gaps	ING TO		Sequence 18, Aj Sequence 28, Aj Sequence 28, Aj Sequence 28, Aj Sequence 28, Aj Sequence 28, Aj Sequence 46, Aj Sequence 46, Aj Sequence 46, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 23, Aj Sequence 19, Aj
	PROTEUS MIRABIL		0;	YTEBSIELLA		Appl Appl Appl Appl Appl Appl Appl Appl

Query Match

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                                                                                                         RESULT 5
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                                     GENERAL INFORMATION:
                                                       Sequence 20403, Application US/09252991A Patent No. 6551795
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GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PARUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4532, Application US/09543681A Patent No. 6605709
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LENGTH: 473
TYPE: PRT
ORGANISM: Klebsiella
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Best Local :
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LENGTH: 480
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APPLICANT: GARY BRETON
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Matches 8; Conserv
       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05
                   APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                             Local
       OF INVENTION:
                                                                                                                                                            139 LTAFFLEA 146
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Rubenfield et al.
NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Best Local Similarity
Matches 8; Conserv:
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US-09-252-991A-20403
                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                    Sequence 42,
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LENGTH: 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wizemann, Theresa M.
APPLICANT: Koenig, Scott
APPLICANT: Johnson, Leslie S
TITLE OF INVENTION: Derivatives of Choline Binding Proteins for Vaccines
FILE REFERENCE: 469201-396
                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 469201-396
CURRENT APPLICATION NUMBER: US/09/286,981B
CURRENT FILING DATE: 1999-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 431
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                          KKEELTS 80
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                                                                                                                                              McDaniel, Larry S.
Swiatlo, Edwin
Yother, Janet
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100.0%; Pred. No.
tive 0; Mismatc
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ADDRESSEE: Curtie STREET: 530 Fifth CITY: New York STATE: New York

E: Curtis, Morris & Safford, P.C. 530 Fifth Avenue

COUNTRY:

U.S.

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US-08-714-741-46
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INFORMATION FOR SEQ ID NO: 42
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
TITLE OF INVENTION: PORTIONS AND PRODUCTS
TORRESPONDENCES: 47
CORRESPONDENCE ADDRESS:
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FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                STREET:
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APPLICATION NUMBER: FILING DATE: 16-SEF CLASSIFICATION: 435
                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08714741
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                                                                                                                                                                                                                                                                                                                                                                  Crain, Marilyn J.
Hollingshead, Susan
Tart, Rebecca
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Swiatlo, Edwin
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212) 840-0712
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                  16-SEP-1996
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                                  US/08/714,741
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Pred. No.
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-714-741-40
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                                                                                                    TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION 15/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
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TOPOLOGY: linear
MOLECULE TYPE: amino acid
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LENGTH: 605 amino acids
TYPE: amino acid
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Local Similarity 100.0%; F
hes 7; Conservative 0;
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REFERENCE/DOCKET NUMBER: 45431
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STATE: New York
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                                                 STRANDEDNESS:
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                                                                                      ENGTH:
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                                                                     amino acid
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                                                                                      864 amino acids
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Crain, Marilyn J.
Hollingshead, Susan
Tart, Rebecca
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Swiatlo, Edwin
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                                                   single
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; Pred. No.
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              RESULT 11
US-09-513-999C-4343
; Sequence 4343, Application US/09513999C
; Patent No. 6783961
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GENERAL INFORMATION:
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Best Local Similarity
Matches 7; Conserv
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INFORMATION FOR SEQ ID NO: 41:
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APPLICANT: Tart, Reb
APPLICANT: Brooks-Wa
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1231 amino acids
TYPE: amino acid
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TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 45431
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STATE: New York
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Hollingshead, Susan
Tart, Rebecca
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Swiatlo, Edwin
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                                                                                                                                                                                                      Score 7; Pred. No.
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; FEATURE:
; NAME/KEY: SIGNAL;
; LOCATION: -36..-1;
; OTHER INFORMATION: 8
; OTHER INFORMATION: 8
; OTHER 1990-4343
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US-09-621-976-5794
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US-09-270-767-57083
; Sequence 57083, Application US/09270767
; Patent No. 6703491
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57083
LENGTH: 56
TYPE: PRT
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FILE REFERENCE: 59. US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
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Best Local Similarity
Matches 6; Conser
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SEQ ID NO 4343
LENGTH: 51
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                                                                                                                                                                                    Sequence 5794, Application US/09621976 Patent No. 6639063
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Best Local :
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               APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENEST.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
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TYPE: PRT
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Patent.pm
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seq LLCYPGWSAVAQS/QL
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100.0%; Pred. No. 11;
tive 0; Mismatches
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                                                               ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-41841
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US-09-270-767-41841
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US-09-134-001C-5232
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; NAME/KEY: SIGNAL
; LOCATION: -53..-1
US-09-621-976-5794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 5232
LENGTH: 134
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.6%; Score 6; DB: Best Local Similarity 100.0%; Pred. No. 25. Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.6%; Score 6; DB 4; Best Local Similarity 100.0%; Pred. No. 19; Matches 6; Conservative 0; Mismatches
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LENGTH: 97
Query Match 14.6%; Score 6; DB 4; Best Local Similarity 100.0%; Pred. No. 27; Matches 6; Conservative 0; Mismatches
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Patent No. 6380370
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ORGANISM: Homo eapiens
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Search completed: February 1, 2005, 15:35:43 Job time : 17.5556 secs This Page Blank (uspto)

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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36 88 77 77 77	Score
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US-10-128-558-167 US-10-282-122A-70087 US-10-282-122A-68101 US-10-299-636-103 US-10-299-636-103 US-09-748-875-4 US-09-748-875-14 US-09-748-875-14 US-09-748-875-14 US-09-298-523B-14 US-09-298-523B-14 US-09-298-523B-14 US-09-298-523B-14 US-09-298-523B-63	ID
Sequence 167, App Sequence 70087, A Sequence 68101, App Sequence 13, Appli Sequence 4, Appli Sequence 4, Appli Sequence 14, Appl Sequence 14, Appl Sequence 97, Appl Sequence 95, Appl Sequence 63, Appl Sequence 63, Appl	Description

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US-10-032-201B-109	US-10-767-701-61193	US-10-424-599-204559	US-10-424-599-162535	US-10-276-774-1710	-10-424-599-25700	US-10-425-115-189548	US-10-029-386-29893	-10-425-115-	US-10-425-115-299684	-10-425-	-10-425-115	US-10-425-115-216216	US-10-227-577-1049	US-10-091-504-1049	US-09-764-891-5371	US-09-764-869-1049	US-10-437-963-136574	US-10-299-636-94	US-09-298-523B-60	US-09-748-875-60	US-10-291-265-459	US-09-298-523B-3	US-09-748-875-3	US-09-298-523B-2	US-09-748-875-2	US-09-298-523B-62	US-09-748-875-62	US-09-298-523B-1	US-09-748-875-1	US-09-298-523B-61	US-09-748-875-61
Sequence 109, App	Sequence 61193, A	Sequence 204559,		Ø	Œ	Ø	Sequence 29893, A				Ø	Sequence 216216,	1049,	Sequence 1049, Ap	e 5371,	~	136	94,	e 60,	60, A	459	Sequence 3, Appli	'n	(P  2)	,	е 6	62,	e 1,	1, ,	ce 61	Sequence 61, Appl

#### ALIGNMENTS

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US-10-128-558-167

Sequence 167, Application US/10128558

Publication No. US20040219521A1

GENERAL INFORMATION:

APPLICANT: Hang, Zhiwei

APPLICANT: Hang, Zhiwei

APPLICANT: Weng, Gezhi

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APPLICANT: Doyle, Bryan J

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LENGTH: 443
TYPE: PRT
ORGANISM: Pseudomonas syringae
US-10-282-122A-70087
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Thes 8; Conservative
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Matches 36; Conserv
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SOPTWARE: pt FL genes Version 6.0
SEQ ID NO 167
LENGTH: 1149
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
EQ ID NO 70087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 NHMGPFMSILQEHIGVMKKEELTSHQSQLTAFFLEA 879
34 LTAFFLEA 41
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Trawick, John
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
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                                                     19.5%; Score 8; DB
100.0%; Pred. No. 2.
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                                                                                                                                                     US-10-299-636-103
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US-10-282-122A-68101
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                                                                                                   Sequence 103, Application No. US200 GENERAL INFORMATION:
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Best Local
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                                  APPLICANT:
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR ADDITOR: 2000-05-26
PRIOR ADDITOR: 2000-05-26
 APPLICANT:
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                                                                    APPLICANT:
                                                                                  APPLICANT: Briles, David E
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-11-27
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Carr, Grant
Carr, Robert
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            Yother, Janet
Crain, Marilyn J
                                McDaniel, Larry
Swiatlo, Edwin
Yother, Janet
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
Hollingshead,
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                                                                                                                     Application US/10299636 o. US20040077847A1
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Mismatches
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US-09-748-875-4
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CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 08/714,741
PRIOR FILING DATE: 1996-09-16
PRIOR APPLICATION NUMBER: 08/529,055
PRIOR FILING DATE: 1995-09-15
PRIOR FILING DATE: 1995-09-15
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patentin Ver. 2.1
Sequence 4, Application US/09748875
Publication No. US20010016200A1
GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT APPLICATION NUMBER: US/09/748,875
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
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LENCTH: 431
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
S-10-254-995-3
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LENGTH: 336
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
S-10-299-636-103
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Best Local (
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APPLICANT: Kcenig, Scott
APPLICANT: Kcenig, Scott
APPLICANT: Johnson, Leslie S
TITLE OF INVENTION: Derivatives of Choline Binding Proteins for Vaccines
FILE REFERENCE: 469201-396
CURRENT APPLICATION NUMBER: US/10/254,995
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/09/286,981
PRIOR APPLICATION NUMBER: US/09/286,981
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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Local Similarity 100.0%; Pred. No. 27
1es 7; Conservative 0; Mismatches
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RESULT 8
US-09-748-875-14
; Sequence 14, Application US/09748875
; Publication No. US20010016200A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
                                                                                                                                  TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 589
TYPE: PRT
ROANISM: Streptococcus pneumoniae
US-09-748-875-14
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SEQ ID NO 4
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Best Local Similarity
Matches 7; Conserv
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 4
LENGTH: 496
                                                                  Best Local Similarity
Matches 7; Conserv
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CURRENT APPLICATION NUMBER: US/09/298,523B
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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324 KKEELTS 330
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                                 KKEELTS 29
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                                                                   Conservative
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                                                              17.1%; Score 7; DB 5
100.0%; Pred. No. 45;
tive 0; Mismatches
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RESULT 11
US-10-299-636-95
; Sequence 95, Application US/10299636
; Publication No. US20040077847A1
; GENERAL INFORMATION:
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Best Local Similarity
"~~ hes 7; Conserve
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NUMBER OF SEQ ID NOS: 111
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 97
LENGTH: 589
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                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/299,636
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 08/714,741
PRIOR FILING DATE: 1996-09-16
PRIOR APPLICATION NUMBER: 08/529,055
PRIOR APPLICATION NUMBER: 08/529,055
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CURRENT APPLICATION NUMBER: US/09/298,523B
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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                                                                                                                            KKEELTS 330
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Crain, Marilyn J
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Swiatlo, Edwin
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100.0%; Pred. No.
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GENERAL INFORMATION:

APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPI
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 63
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US-09-298-523B-63
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US-09-748-875-63
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Sequence 63, Application US/09298523B
publication No. US20030059438A1
GENERAL INFORMATION:
APPLICANT: BRILES et al.
APPLICANT: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/298,523B
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Publication No. US20010016200A1
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CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 08/714,741
PRIOR FILING DATE: 1996-09-16
PRIOR FILING DATE: 1996-09-16
PRIOR APPLICATION NUMBER: 08/529,055
PRIOR FILING DATE: 1995-09-15
NUMBER OF SEQ ID NOS: 111
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
FILE REFERENCE: 57909/361
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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Tart, Rebecca
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Crain, Marilyn J
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Swiatlo, Edwin
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100.0%; Pred. No. 51;
Live 0; Mismatches
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RESULT 14

US-09-748-875-61

US-09-748-875-61

Sequence 61, Application US/09748875

Publication No. US20010016200A1

GENERAL INFORMATION:
APPLICANT: BRILES et al.

APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS

TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR

FILE REFERENCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 61
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NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 63

LENGTH: 670

TYPE: PRT

ORGANISM: Streptococcus pneumoniae
US-09-298-523B-63
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US-09-298-523B-61
J Sequence 61, Application US/09298523B
Publication No. US2003005943BA1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT BRILES et al.
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-61
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APPLICANT: BRILES et al.

APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS

TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR

FILE REFERENCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/298,523B

CURRENT FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 61

LEUGTH: 690

TYPE: PRT

CORANISM: Streptococcue pneumoniae
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                                                                      Matches
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                                                                 y Match 17.1%; Score 7; DB 10; Length 690;
Local Similarity 100.0%; Pred. No. 52;
nes 7; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 52;
es 7; Conservative 0; Mismatches
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23 KKEELTS 29
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Db 361 KKEELTS 367

Search completed: February 1, 2005, 15:44:48 Job time: 59.7778 secs

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Title: Perfect score: SEQ5VAL1854

Scoring table: Sequence: Gapop 60.0 , Gapext 60.0 OLIGO EKNWKNHMGPFMSILQEHIG.....MKKEELTSHQSQLTAFFLEA 41

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: Word size : 0 279530

Minimum DB seq length: 21
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Regult No			Length 467 488 488 276 217 417 417 417 40 60 1196 1147 81 1107 1134 1131 1131		
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18	ტ	•	189	N	H96520
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21	6	٠.	228	N	AC3204
22	O	14.6	237	N	G70066
23	6	14.6	241	N	G97416
24	6	14.6	241	N	AI26
25	6	14.6	274	H	F40362
26	ტ	٠	276	N	S27641
27			280	N	
28	6				D861
	თთ	14.6	351	N	D86193 T03153

A;Cross-references: UNIPROT:007440; EMBL:Y10528; NID:g2208963; PIDN:CAA71555.1; PID:g220 A;Experimental source: strain PAO1, substrain PAO6049 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-488 <CUN>

R;Cunningham, L.; Pitt, M.; Williams, H.D.
Mol. Microbiol. 24, 579-591, 1997
Mol. Microbiol. 24, 579-591, 1997
A;Title: The cioAB genes from Pseudomonas aeruginosa code for a novel cyanide-insensitiv A;Reference number: Z24440, MUID:97323403; PMID:9179851
A;Accession: T47273

cyanide insensitive terminal oxidase chain cloA [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004 C;Accession: T47273; G83155

45	44	43	42	41	40	39	38	37	36	U S	υ 4	ω U	32	31	30
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T04265	F83759	A83370	T30911	B90419	E86616	D72008	B81531	S00985	S33681	FIMS4A	S30278	S13269	E96972	AD1937	S76427
probable kasein ki	cytochrome d (bd-t	probable MFS trans	xylanase (EC 3.2.1	hypothetical prote	CT850 hypothetical	CT850 hypothetical	conserved hypothet	translation initia	translation initia	translation initia	translation initia	translation initia	riboflavin biosynt	permease protein o	hypothetical prote

# ALIGNMENTS

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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2g17780 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84556
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A;Residues: 1-488 <STO>
A;Cross-references: GB:AE004810; GB:AE004091; NID:g9950106; PIDN:AAG07317.1; GSPDB:GN00:
                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1997
A;Reference number: Z16500
A;Accession: T08859
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C;Superfamily: cytocl
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A; Introns: 137/3
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A; Residues: 1-276 <WAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translated from GB/EMBL/DDB
                                                                                                                                ;Molecule type: DNA;Residues: 1-417 <STO>;Cross-references: GB:
                                                                                                                                                                                         Status: preliminary
                                                                          Gene: At2g17780
Map position: 2
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   Matches
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 Similarity 7; Conserv
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8; Conserv
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17.1%; Score 7; DB larity 100.0%; Pred. No. 7. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                  GB:AE002093; NID:g6598810; PIDN:AAB80787.2; GSPDB:GN00139
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100.0%; Pred. No. 5.4;
Live 0; Mismatches
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lo. 0.75;
                   DB 2;
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Query Match
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Thes 7; Conserve
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A;Superfamily: cytochrome d complex terminal oxidase chain I C;Keywords: oxidoreductase
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                                                                                                                                                                               A;Introns: 33/3; 66/3; 261/2; 299/3; 479/2; 615/3; 750/3; 903/2; 925/3 C;Superfamily: Caenorhabditis elegans F44B9.6 protein
                                                                                                                                                                                                                                                   A;Cross-references: EMBL:L23648; NID:g388585; PID:g388591
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J. Bacteriol. 173, 6230-6241, 1991
A;Title: Cloning, characterization, and expression in Escherichia coli of the genes enco A;Reference number: A38170; MUID:92011387; PMID:1655703
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                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-960 < ANT>
                                                                                                                                                                                                                                                                                                                                               A; Accession: S44812
                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, September 1993
A;Description: Sequence of the C. elegans cosmid F
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A;Molecule type: DNA
A;Residues: 1-13 <MO2>
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A;Molecule type: DNA
A;Residues: 1-537 <MOS>
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                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                       ;Reference number: S44807
                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Antonacci-Fulton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Mar-2000
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                                         ELTSHQS 32
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H86389
photosystem I chain IX - Cyanophora paradoxa cyanelle C;Species: cyanelle Cyanophora paradoxa C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C;Accession: T06840 R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryan submitted to the EMBL Data Library, July 1995
                                                                                                                                                                  RESULT 9
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R;Lang, B.F; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, Nature 387, 493-497, 1997
Nature 387, 493-497, 1997
A;Title: An ancestral mitochondrial DNA resembling a eubacterial A;Reference number: S78127; MUID:97311393; PMID:9168110
A;Accession: S78131
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C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1478 <LAN>
A;Residues: 1-1478 <LAN>
A;Cross-references: UNIPROT:O21237; EMBL:AF007261; NID:g2258325; PIDN:AAD11864.1;
A;Experimental source: ATCC 50394
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A; Residues: 1-1196 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: DNA-directed RNA polymerase beta chain (Keywords: mitochondrion; nucleotidyltransferase; tr
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7; Conserv
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100.0%; Pred. No.
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A; Cross-references: UNIPROT: P73857; A; Note: the nucleotide sequence was

EMBL:D90910; submitted to

GB:AB001339; NID:g1652956; PIDN:BAA17910 the EMBL Data Library, June 1996

A;Start

codon: GTG

Genetics:

Query Match Best Local (

Matches

Similarity 6; Conserv

14.6%; ilarity 100.0%; Conservative

0

0 Length

Indels

0

Gaps

0

Score 6; DB 2 Pred. No. 20; 0; Mismatches

DB . 20;

2;

A; Molecule type: DNA A; Residues: 1-75 < KAN>

A;Status: nucleic acid sequence

not

shown;

translation PMID:8905231

not

A; Reference number: S74322; MUID: 97061201; A; Accession: S75054

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R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04666
                                  C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 (C;Accession: S75054 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; lo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamad DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: C; Genetics:
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                  C;Species: Synechocystis sp
A;Variety: PCC 6803
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A; Residues: 1-69 < TYB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: photosystem I protein psaJ
C;Keywords: cyanelle; photosynthesis; photosystem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: psaJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P48117; EMBL:U30821; NID:g1016083; PIDN:AAA81183.1; PID:g101
A;Experimental source: strain Pringsheim LB555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-40 <STI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z15840
A; Accession: T06840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: Nucleotide sequence of the cyanelle genome
                                                                                                                                                                           hypothetical protein ssl3127 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                             14.6%;
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                                                                                                                                                                           Synechocystis sp.
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                                                                                                                                                                                                                                                                                                                                                                                               Length 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (fragment)
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                                                                                                                                                                                                                                                                                                                                                          Indels
                                                       , E.; Nakamura, Y.; Miyajima, N.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                             DOG
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T46439

hypothetical protein DKFZp434M0326.1 - human

C;Species: Homo sapiens (man)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46439
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A;Residues: 1-134 <KANN>
                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P73195; EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAA1722
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: ferredoxin [2Fe-28], Clostridium type
C;Keywords: 2Fe-28; electron transfer; iron-sulfur protein; metalloprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakao, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, DNA Res. 3, 109-136, 1996
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Biochemistry 26, 1209-1214, 1987
Biochemistry 26, 1209-1214, 1987
A;Title: The primary structure of thioredoxin from Chromatium vinosum determined by high A;Reference number: A26622; MUID:87185419; PMID:3567166
A;Accession: A26622
                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S74322; MUID:97061201; A;Accession: S75307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P09857
A;Note: unidentified residues are Ile or Leu
C;Superfamily: Thioredoxin; thioredoxin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Chromatium vinosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: heat-stable protein; redox-active disulfide F;10-93/Domain: thioredoxin homology <THR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-107 < JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erredoxin [2Fe-2S] sll1584 [similarity] - Synechocystis sp. (strain PCC 6803); Species: Synechocystis sp. (variety: Synechocystis sp. (variety: PCC 6803); Variety: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004; Accession: S75307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;32-35/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                    32,40,80,84/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A26622
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100.0%; Pred. No
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o. 28;
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Search completed: February Job time: 13.5556 secs

μ,

2005, 15:33:02

: 13.5556 весв

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A;Molecule type: DNA
A;Residues: 1-143 <570>
A;Cross-references: UNIPROT:Q9Z6J0; GB:BA000008; NID:g8979442; PIDN:BAA99276.1; GSPDB:GN:
A;Experimental source: strain J138
C;Genetics:
                                                                                                                                                                                                                                           C;Accession: B86624
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86624
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
B86624
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                             S
                                                                                                                                 A;Gene:
                                                                                                                                                                                                                                                                                                                                               HTH transcription regulator [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A;Residues: 1-137 <ANA>
A;Cross-references: UNIPROT:Q9NSX2; EMBL:AL137681
A;Experimental source: adult testis; clone DKFZp434M0326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z23028
A; Accession: T46439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000
                                                                  Matches
                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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75
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                                                                                Similarity
SILOEH
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80
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                                                             Score 6; DB 2; Pred. No. 36; 0; Mismatches
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35;
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H .; 181

Run on:

Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd

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Scoring table:
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Perfect score:
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seq length: 2000000000
  Match Length DB
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Q6N0G9
Q73H35
CAE30233
AAS14431
Q8PG82
Q8P4L6
Q8P4L6
Q8BE17
Q8PMA6
                                                                                                   Q89NV6
Q8P701
Q8Z912
                                                                                                                               Q7NRX0
Q98DW1
Q87H28
Q7WBI0
Q7WN02
Q7WN02
Q8XQI3
Q8XQI3
                                                                                                                                                                                                     Q8BIC5
Q8BIJ2
Q7N5B2
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334.352 Million cell updates/sec
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               Aas14431 wolbachia
Ospg82 xanthomonas
Ospg82 xanthomonas
Osp416 xanthomonas
Osp416 yanthomonas
                                                                                       Q7nrx0 Chromobacte
Q98dw1 rhizobium 1
Q87h28 vibrio para
Q7wbi0 bordetella
Q7wn02 bordetella
Q8xqi3 ralstonia s
O86080 rhodobacter
Q89nv6 bradyrhizob
Q89701 xanthomonas
Q82912 salmonella
Q8zq3 salmonella
                                                                                                                                                                                                     Q8bic5 mus musculu
Q8bij2 mus musculu
Q7n5b2 photorhabdu
                                                                                                                                                                                                                                             Q96es5 homo sapien
Q8n717 homo sapien
Q6p197 homo sapien
                                                                                                                                                                                                                                                                                               Q9gm44 macaca fasc
Q9h583 homo sapien
                                                                    Q6n0g9 rhodopseudo
Q73h35 wolbachia p
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Q8cct5 mus musculu
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RESULT 2
BP28_HUMAN
ID BP28_HUMAN S'
AC Q9H583; Q9NW23;
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Result

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STANDARD;

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2144 AA

Minimum Maximum

Searched:

sequence:

45	44	43	42	41	40	39	38	37	36	35	34	W	32
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17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	19.5	19.5	19.5
545	537	525	525	482	464	460	417	405	296	258	493	488	488
N	_	N	N	N	N	N	N	N	N	N	N	N	N
Q6BUSS	CYDA_AZOVI	Q88UI6	Q8GZTS	Q8XQL5	Q8NKT5	Q7Z9N1	Q9NVT4	Q8GF00	Q8S312	Q88E22	Q92S67	Q7DC90	007440
Q6bu55	Q09049	Q88ui6	Q8gzt5	Q8xq15	Q8nkt5	Q7z9n1	Q9nvt4	Q8gf00	Q8s312	Q88e22	Q92s67	Q7dc90	007440
debaryomyce	azotobacter	lactobacill	emiliania h	ralstonia s	acidianus a	trichoderma	homo sapien	clostridium	phytophthor	pseudomonas	rhizobium m	pseudomonas	pseudomonas

### ALIGNMENTS

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Matches 41
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                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       EMBL; AB049842; BAB16728.1; ALT_INIT.
InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                     libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the BAP28 family.
-!- SIMILARITY: Contains 1 HEAT repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Tanuma R., Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca. NCBI_TaxID=9541; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                      SEQUENCE
                                                                                                                                                                                   PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=BAP28;
648
                                                                                   Similarity
                  EKNWKNHMGPFMSILQEHIGVMKKEELTSHQSQLTAFFLEA 41
EKNWKNHMGPFMSILQEHIGVMKKEELTSHQSQLTAFFLEA
                                                                                                                                      958 AA; 108644 MW;
                                                                                                                                                        920
                                                                 100.0%; Score 41; DB 1; 1 larity 100.0%; Pred. No. 9.8e-36; Conservative 0; Mismatches 0;
                                                                                                                                                         956
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                                                                                                                                      3DBD95C3623CFB31 CRC64;
                                                                                                   Length 958;
                                                                    Indels
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RX PubMed-14702039; DOI-dl.1038/ngl285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sugamart K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Xodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Xodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Cmura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimitu F., Wakabe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takencto M., Chori Y., Suzuki O.,
RA Nakagawa S., Senoh R., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kumazaki M., Watanabe T., Kobatake N., Inagami A., Fujiwara T.,
RA Kuwabata A., Hikiji T., Kobatake N., Inagaki H., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Masuho Y., Yamashita R.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Masuho Y., Yamashita R.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Masuho Y., Yamashita R.,
RA Makajaki K., Wataima M., Satoh T., Shirai Y., Masuho Y., Yamashita R.,
RA Makajaki K., Nagase T., Nomura Y., Ohara O., Isogai
                                                                                                         EMBL; AX067150; CAC26776.1;
EMBL; AL136105; CAC15948.1;
EMBL; AK001221; BAA91564.1;
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
Polymorphism.
REPEAT 2106
                              SWISS-2DPAGE; Q9H583; HUMAN.
InterPro; IPRO08938; ARM.
InterPro; IPRO00357; HEAT.
PROSITE; PSS0077; HEAT_REPER
                                                                                                                                                                                                          use by non-profit institutions as modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel BAP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                            . Genet. 36:40-45(2004).
SIMILARITY: Belongs to the BAP28 far
SIMILARITY: Contains 1 HEAT repeat.
                                PSS0077; HEAT_REPEAT; FALSE_NEG.
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r WO0100669,
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Primates;
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Last sequence
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, 04-JAN-2001.
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annotation update)
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ein.":
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X MEDLINE-22388257; pubMed-12477932;

X Strausberg R.L., Feingold E.A., Couse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

XA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

XA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

XA Brownstein M.J., Wodin T.B., Toshiyuki S., Garninci P., Prange C.,

XA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XA Richards J., Holon E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

XA Milialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XA Milialon S., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

XA Maritin M. Madan A. Ponnga A.C., Sheychenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   777777
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Q8VCK1;
01-MAR-2002
01-MAR-2002
                                                                                                         Submitted (DEC-2001) to the ENEMBL, BC019693, IAH19693, I; -
MGD; MGI:3384983; BC019693,
InterPro; IPR008938; ARM,
SEQUENCE 349 AA; 40166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                          STRAIN=mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                       Tones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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llarity 100.0%;
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Rodentia;
                            63.4%;
                                                                                                                                                                                                                                                                        WAP-TGF alpha model. 7 months old;
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Score 26; DB; Pred. No. 8.4.0; Mismatches
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Pred. No. 2e-35;
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Matches

26;

Conservative

0,

DB 2;

Length 349

Indels

0

Gaps

0,

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Similarity

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Q8CCT5;
Q8CCT5;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430400D06 product:hypothetical ARM repe
structure containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Olfactory
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                    brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408
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                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae;
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STRAIN-C57BL/6J; TISSUE-Olfactory brain; MEDLINE-21085660; PubMed-11217851; SEQUENCE FROM N.A. STRAIN=C57BL/6J; T "Functional annotation of a full-length mouse cDNA collection."; RIKEN FANTOM Consortium; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Enzymol. 303:19-44(1999)

the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.", Nature 420:563-573(2002). SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Olfactory FANTOM Consortium brain annotation of Team;

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Olfactory brain;
MEDLINE=20499374; PubMed=11042159;
Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000). Shibata K., Itoh **≾** 

genes."

SEQUENCE FROM N.A.

STRAIN-CS7BL/GJ, TISSUE-Olfactory brain;
STRAIN-CS7BL/GJ, TISSUE-Olfactory brain;
STRAIN-CS7BL/GJ, TISSUE-Olfactory brain;
STRAIN-CS7BL/GJ, TISSUE-Olfactory brain;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).

FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P. Piukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirakaka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., STRAIN-C57BL/6J; TISSUE-Olfactory brain; .0

μ

EKNWKNHMGPFMSILQEHIG

Similarity

.0%;

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.8e-13;

Indels

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Conservative

RESULT Q96ES5 ID QS 밁 S RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeebbarg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeebbarg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wadin T.B., Foters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holden R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RY "Generation and intital analysis of more than 15 000 fell locath human
"Generation and intital analysis of more than 15 000 fell locath human
"Generation and intital analysis of more than 15 000 fell locath human
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"Generation and intital analysis of more than 15 000 fell locath human
"Generation and intital analysis of more than 15 000 fell locath human Query Match Best Local S Matches 20 Matches Query Match Best Local Q96ES5; Q96ES5; 01-DEC-2001 01-DEC-2001 Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y. Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T. Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO32134; BAC27721.; -.

MGD; MGI:2384983; BC019693. EMBL; Hypothetical SEQUENCE 4 InterPro; Submitted Strausberg R.; and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S. MEDLINE=22388257; SEQUENCE FROM N.A. Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens (Human) Name=FLJ10359; FLJ10359 protein. 01-DEC-2001 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel. TISSUE=Ovary; "Generation and initial analysis of more than 15,000 full-length human InterPro; EQUENCE FROM N.A. S SSUE=Ovary; tted (JUL-2001) to the BC011983; AAH11983.1; Pro; IPR008938; ARM. NCE 349 AA; 39921 MY 99 N Similarity KNWKNHMGPFMSILQEHIGVMKKEEL 27 KNWKNHMGPFMSILQEHIGVMKKEEL 124 IPR008938; ARM. al protein. (TrEMBLrel. 19, TrEMBLrel. 19, TrEMBLrel. 25, 63.4%; llarity 100.0%; Conservative PubMed=12477932; Chordata; Primates; 39921 MW; 46688 MW; to the EMBL/GenBank/DDBJ databases 48.8%; 100.0%; Last Last Score 20; ; Pred. No. 0; Created) Score 26; Pred. No. Craniata; Vertebrata; I Catarrhini; Hominidae; 99:16899-16903 (2002). 3A359597FF7079EB CRC64 42AB9EB13CA3FE67 CRC64 Mismatches annotation sequence update) 349 DB 2; DB 2; 9.6e-8 update) Length 349; Length 408; Indels Euteleostomi; 0 Tagami Gaps .B.Y.S. 0

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EKNWKNHMGPFMSILQEHIG

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RESULT 7
Q6P197
ID Q6P1
AC Q6P1
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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Satto K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Satto K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Ishima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Ishihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Ono T., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohmori Y.,
RA Atsamara K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizuhima S., Satoh T., Shirai Y., Nakagawa K.,
RA Mizuhima S., Satoh T., Shirai Y., Nakagawa K.,
RA Mizuhima S., Satoh T., Shirai Y., Nakagawa K.,
RA Mizuhima S., Satoh T., Shirai Y., Nakagawa K.,
RA Nakagian T., Nakamra Y., Ohara O., Isogai T., Sugano S.,
CDNAs, H., Masuho Y., Yamashita R.,
RA Nakagian T., Nakamara Y., Ohara O., Isogai T., Sugano S.,
CDNAs, H., Masuho Y., Satoh M., Masuho Y., Yamashita R.,
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Q6P197;
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
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01-OCT-2002 (TrEMBLrel. 22, La
01-OCT-2003 (TrEMBLrel. 25, La
01-OCT-2003 (TrEMBLrel. 25, La
Hypothetical protein FLJ40893.
                            FLJ10359 protein (Fragment)
Name=FLJ10359;
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ilarity 100.0%;
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      (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101574 MW;
                                                                                         27,
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22, Last sequence update)
25, Last annotation update)
                                                                                         Last
Last
                                                                                                                                                       Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                           606
                                                                                                                                                                                                                    PRT;
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                                                                                                                   sequence update)
                                                                                             annotation update)
                                                                                                                                                                                                                    1106
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RESULT 8
AAH65205
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Stapleton M., Gudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Ra Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Ra Bobak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Raha S.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                             AAH65205;

02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last seq
02-MAR-2004 (TrEMBLrel. 27, Last ann
PL-110359 protein (Fragment).
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008938;
NON TER 1
SEQUENCE 1106 AA;
                                                       FLJ10359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2004) to the EMBL; BC065205; AAH65205.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.;
"Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                         AAH65205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                         PRELIMINARY;
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100.0%; Pr
   Primates;
                 Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                       125359 MW;
                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 7.6e-
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 8

AAH65205

AAH65205

AAH65205;

AC AAH65205;

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

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DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last
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Best Local
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STRAIN=C57BL/6J;

MEDLINE=20499374; PubMed=11042159;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Carninci P., Shibata Y., Muramatsu M., Hayashizaki Y.;

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected "Normalization and subtraction of cap-trapper-selected "Normalization and subtraction of cap-trapper-selected"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8BIC5;
Q8BIC5;
01-MAR-2003
01-MAR-2003
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full
length enriched library, clone:F730048A22 product:weakly similar
length enriched library, Clone:F730048A22 product:weakly similar
BA393016.3 (NOVEL KRAB BOX CONTAINING ZINC FINGER GENE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.
                                                                                                                                                                                                        60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o
                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-BB114266;
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium;
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c. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 796
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                                                                                                                                                                                                                                                                                                                                                                                                      409:685-690(2001).
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                                                                                                                                                           FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cy full-length cDNA cloning.";
303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Chordata; ; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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7.6e-1
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                                                                                                                                                                                                                                                       p Phase I & II
on functional
                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA collection.";
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                                                                                     Shibata
            of new ge
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A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
K Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
B MSD, AKO89532; BBC40916.1; -.
BMSL; AKO89532; BBC40916.1; -.
BMSL; PL5822; 1BBC.
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuncto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000)
                                                  SEQUENCE FROM N.A. STRAIN=C57BL/6J; MEDLINE=99279253;
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003676; F:nucleic acid binding;
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR007087; Znf_C2H2.
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                                                             PubMed=10349636;
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Rodentia;
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RIKEN full-length enriched library,
akly similar to BA393J16.3 (NOVEL KF
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Sciurognathi; Muridae; Murinae; Mus
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R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0005676; F:nucleic acid binding; IEA.
R GO; GO:0008270; F:zinc ion binding; IEA.
R GO; GO:0008270; F:zinc ion binding; IEA.
R GO; GO:0008270; F:zinc ion binding; IEA.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent interpro; IPR00190; KRAB.
Interpro; IPR00190; KRAB; 1.
R Pfam; PF01352; KRAB; 1.
R Pfam; PF00096; zf-C2H2; 7.
R PF00096; zf-C2H2; 7.
R PF00096; zf-C2H2; 7.
R SMART; SM00349; KRAB; 1.
R SMART; SM00355; ZNF-C2H2; 7.
R PROSITE; PS0085; ZNC_FINGER-C2H2_1; 7.
R PROSITE; PS0157; ZINC_FINGER-C2H2_1; 7.
R PROSITE; PS50157; ZINC_FINGER-C2H2_1; 7.
R PROSITE; PS50157; ZINC_FINGER-C2H2_1; 7.
R PROSITE; PS50157; ZINC_FINGER-C2H2_1; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashiz Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AK049344; BAC33696.1; -. HSSP; P08046; 1F2I.
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the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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RIKEN FANTOM Consortium;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016118; P:electron transport; IEA.
InterPro; IPR002585; Bac_Ubq_Cox.
Pfam; PP01654; Bac_Ubq_Cox; I.
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OrderedLocusNames=plu2043;
Photorhabdus luminescens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Photorhabdus.
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SEQUENCE FROM N.A.
STRAIR-ATCC 12472 / DSM 30191;
MEDLINE=22882880; PubMed=14500782;
Vasconcelos A.T.R., de Almeida D.F., Hu
Antonio R.V., Almeida F.C., de Almeida
                                                                                                                         Cyanide insensitive terminal oxidase Name=cioA; OrderedLocusNames=CV3658;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                      NCBI_TaxID=536;
                                                                                    Bacteria; Proteobacteria; Betaproteobacteria; Neisseriaceae; Chromobacterium.
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EMBL; BX571865; CAE14336.1;
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01-MAR-2004
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RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
Carvallo C.M.B., Cascardo J.C.M., Carvada B.S., Chueire L.M.O.,
RA Carvallo C.M.B., Cascardo J.C.M., Cavada B.S., Clueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Parto M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Jardim S.N., Laurino J.,
RA Gazzinelli C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA Macimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Macimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Parixa M.M.R., da Silva A. B.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
Silva A.M.R., da Silva A. B.C., Silva D.W., Silva R., Simoes I.C.,
RA Silva A.M.R., Garses R.B.A., Souza E.M., Souza K.R.L.,
Shon D., Soares C.M.A., Soares R.B.M., Souza K.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,
Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
RMI Froct Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
RMI Froct Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RMGO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016491, Boc Ung Cox. T.
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01-OCT-2001 (TrEMBLrel. 18, C
01-OCT-2001 (TrEMBLrel. 18, L
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Quinol oxidase subunit I.
                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato 1 Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing Mesorhizobium loti (supplement)."; DNA Res. 7:381-406(2000).
                                    SEQUENCE FROM N.A. STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MAFF303099;
MEDLINE=21082936; PubMed=11214974;
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Phyllobacteriaceae, Mesorhizobium.
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Rhizobium loti (Mesorhizobium loti).
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PubMed=11214968;
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Lancet 361:743-749(2000),
EMBL, APO05088; BAC62480.1; -...
GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016491; F:oxidoreductase activity; IE
R GO; GO:0006118; P:electron transport; IEA.
T-*--Pro; IPR002585; Bac Ubq_Cox.
T-*--Pro; IPR002585; Bac Ubq_Cox.
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DNA Res. 7:331-338(2000).

EMBL; AP003004; BAB51159.1; -.

GO; GO:0016491; F:oxidoreductase activity; IE
GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR002585; Bac_Ubg_Cox.

Pfam; PF01654; Bac_Ubg_Cox; 1.

Complete proteome.
Q7WBI0;
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01-OCT-2003
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SEQUENCE
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MEDLINE=22508454; PubMed=12620739;
Makino K., Obhima K., Kurokawa K., Yokoyama K., Uda T., Ta
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
'Genome sequence of Vibrio parahaemolyticus: a pathogenic
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
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Q87H28;
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01-JUN-2003 (TrEMBLrel. 24,
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Cytochrome BD2, subunit I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
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82 STRAIN=12822 / ATCC BAA-587;

83 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

84 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

85 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

86 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

87 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

88 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

89 WEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

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Best Local Similarity 100.0%; Pred. No. 4;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; P:electron transport; IEA.
InterPro; IPR002585; Bac_Ubq_Cox.
Pfam; PF01654; Bac_Ubq_Cox; I.
Complete proteome.
SEQUENCE 462 AA; 49902 MW; 631FAC87419163ED
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Cytochrome oxidase subunit I.
Name=cloA; Synonyms-qxtA; OrderedLocusNames=BPP1024;
Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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ç	2	82	74	74	72	65	65	65	52	48	36	36	36	36	36	36	32	1150	655	118	378	2144	515	1149	349	Query Match Length
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	ADK34600	AAM92148	ABM52779	AAU56260	ABP07304	ABJ18786	ABU38795	AAU36456	ABO55613	ABU60930	ABG43897	ABG55759	AAM61279	AAM74002	AAM34177	ABB40457	ABB15816	ABB63215	AAE13001	ABM73641	ABU21620	AAB85029	AAW54099	ADE08012	AAB92729	ID
3	Noval		Abm52779 Propionib	-	Abp07304 Human ORF	Abj18786 Pseudomon	Abu38795 Protein e	Aau36456 Pseudomon	Abo55613 Human gen	Lung	Abg43897 Human pep	Abg55759 Human liv	Aam61279 Human bra	Aam74002 Human bon	Aam34177 Peptide #	Abb40457 Peptide #	Abb15816 Human ner	٠.	Aae13001 Rice poly	Abm73641 DNA clone	Abu21620 Protein e	Aab85029 Protein e	Aaw54099 Homo sapi	Ade08012 Novel pro	9 Human p	Description

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8; SEQ ID NO 11159; 2537pp + Sequence Listing; English.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	•	14.6		14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6
164	164	161	150	141	141	141	138	138	132	124	121	108	107	102	102	102	87	86	86
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AAM80897	AAG47182	AAR77507	ADM19866	AAY07240	AAY07241	AAY07239	AAO10626	AAB42068	AAG01565	ADC96770	AA002764	ABG13882	AAB19971	ABU24822	AA017456	AAB76556	ADM26908	ABO78538	AA007992
Aam80897	Aag47182	Aar77507	Adm19866	Aay07240	Aay07241	Aay07239	Aao10626	Aab42068	Aag01565	Adc96770	Aao02764	Abg13882	Aab19971	Abu24822	Aao17456	Aab76556	Adm26908	Abo78538	Aaou/992
	Arabidops	'Human neu	Protein e	Fragment	Fragment		Human pol	Human ORF	Human sec	_	Human pol	Novel hum	. Human STA	Protein e	Human liv	Corynebac	Hyperther	Pseudomon	tuman por

## ALIGNMENTS

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RESULT 1
AAB92729
29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                 Ota T, 1
Ishii S,
                                                                                                                                                                                                                  28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:11159.
                                                                                                                                                                                                                                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                                                                                                       AAB92729 standard; protein; 349
                                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                        (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                EP1074617-A2.
                                                                                                                                 Isogai T, Nishikawa T, Hayashi K, (
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                             99JP-00300253.
2000JP-00118776.
2000JP-00183767.
                                                                                                                                                                       2000JP-00241899
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                                                                                                                                 Saito K, Yamamoto, Otsuki T;
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RESULT 2
ADE08012
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
Claim 20; SEQ ID NO 1078; 1177pp; English.
                                              New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2002;
22-APR-2002;
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11-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein (useful for identifying genetic disorders) #167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE08012;
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DB; ADE07101.
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                                                                                                                                                                                                                                 Asundi V, Goodrich RW,
Xue AJ, Wehrman T, Wer
ng D, Chen R, Xu C, Bc
                                                                                                                                                                                                                                                                                                                                                                                      2001US-0339739P.
2001US-0339453P.
2002US-0365091P.
2002US-0365384P.
2002US-0376381P.
2002US-0372618P.
2002US-0376045P.
2002US-0376045P.
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100.0%; Pred. No. 1.6e-35;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                 RW, Ren F, Zhang J, Zhac
Weng G, Zhou P, Drmanac
Boyle BJ;
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wanac RT,
                                                                                                                                                                                                                                                            Wang
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the invention are useful

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Sequence 515 AA

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03-APR-1997;
04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                 The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, BRCAI, binding proteins BARDI, B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a BARDI, B123, BE2, BE14, BE31 or BE445 mucleic acid sequence, specifically a wild type BARDI composition for the detection or purification of BRCAI, useful to identify a patient having, or at risk of developing cancer. BARDI can be used in the preparation of an anti-BARDI antibody, and in the detection and purification of a BRCAI protein. BARDI, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARDI, B123, BE2, BE14, BE31 or BE445 to BECAI back to the binding of BARDI, B123, BE2, BE14, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE445, BE31 or BE44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens BAP28 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW54099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence encoding BARD1, B123, BE2, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV24135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-230317/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW54099 standard; protein;
                                                                              B123, BE2, BE14, BE31 or BE445 complex. The antibodies can be u
detect BARD1, B123, BE2, BE14, BE31 or BE445, a specific anti-B
antibody can be used to identify a patient having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 287-288; 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patient having or at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowcock AM,
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                                                      developing cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; BRCA1; breast cancer; risk; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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97US-0042611P.
97US-0042985P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41;
100.0%; Pred. No.
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Query Match

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RESULT 4
AAB85029
ID AAB85029
AC AAB8
XX AAB85
XX AAB8
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XX Prot
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Query Match 48.8%; Score 20; Best Local Similarity 100.0%; Pred. No. Matches 20; Conservative 0; Mismatcl
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                                                                                                                                                                                   sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polypucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first cDNA sequence of the BAP28 gene consisting of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization oppolymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barry
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                                                                                                                Sequence 2144 AA;
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                                                                                                               CC polypeptide or its fragment whose expression is inhibited by the care the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for cc proliferation; (7) identifying a compound that influences the activity of cc required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway cc required for proliferation, or that inhibits cellular proliferation of the biological pathway in which a proliferation required gene or its gene product lies compound that inhibits proliferation of an crganism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an compound that inhibits proliferation of an creaming strains in which the gene product is overexpressed of underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the creamining the extent continues or critical proliferation of screening for homologous nucleic acids required content from the proliferation to isolate candidate molecules for rational content for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polyperation of the property of the sequence of the vector of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property 
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 49544; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2002.
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                                                                                          varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                           Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                                                    WPI;
                                          Sequence 118 AA;
                                                                                                                                                                                                                                                   Disclosure;
                                                                      at ftp.wipo.int/pub/published-pct-sequences. (Updated on 23-OCT-2003 to
standardise OS field)
                                                                                                                                                                                                                        The present invention
                                                                                                                                                                                                                                                                                 characteristics.
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27-SEP-2002;
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20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
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17-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                (SNP).
 Local Similarity
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                                                                                                                                                                                            (Hordeum vulgare) which contain single nucleotide polymorphisms
The oligonucleotides may be used for analysis of SNPs among barley
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Takeda K,
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2002JP-00327515.
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 17.1%;
100.0%;
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Score 7;
Pred. No.
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DB 7;
           Length 118;
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RESULT 8 ABB63215 ID ABB6

ABB63215 standard;

protein; 1150

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                                                                                                                              polyadenylated RNA-binding protein or eukaryotic translation initiation factor 4 (eIF-4) gamma. The nucleic acid fragments may be used in PCR protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA, to create transgenic plants in which the new polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. The nucleic acids may also be used as probes for genetic or physical mapping the genes that they are part of and as makers for traits linked to those genes. The polypeptides may be used as makers for traits linked to those to facilitate design and/or identification of inhibitors of those enzymes that can be used as herbicides. The present sequence is rice poly (A) binding protein from clone rsr9n.pk005.117
                                                                                                         Sequence 655 AA;
                                                                                                                                                                                                                                                                                                                           Claim 9; Fig 1-3; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding poly(A) binding protein or a eukaryotic translation initiation factor-4 gamma, useful for creating transgenic plants where the proteins are present at higher or lower levels than
                                                                                                                                                                                                                                                                                                 The present invention relates to an isolated polynucleotide encoding
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583 PLVDQLE 589
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                                                                 17.1%;
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on initiation factor-4 (eIF-4) gamma;
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RESULT 9
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Best Local
Human; nootropic; neuroprotective; cytostatic; dermatological; virus immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnes antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiuleer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventior useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                   Human nervous system related polypeptide SEQ ID
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                                                                                                                                                                                                                                                                ABB15816 standard; protein; 32 AA.
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Matches 6
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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100.0%; Pred. No. 65
cive 0; Mismatches
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MOLECULAR DYNAMICS INC

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Hanzel DK,

Chen W,

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RESULT 11
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Best Local &
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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36
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                                                                                                                                                                  Claim 27;
                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                 expression in human placenta
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                                                                                                                                                            SEQ ID NO 34446; 654pp; English
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                                                                                                                                                                                                                                                                                                                                                       Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00638408.
; 2000US-005323687P.
; 2000US-0236359P.
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6; DB 4; Pred. No. 72; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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RESULT 13 AAM61279

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26-MAY-2000;
30-JUN-2000;
                                                                                              probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human genetic disorders
                                                                                                                                                                                                                                                                                                    03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone marrow expressed probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM74002 standard;
                                                                             Sequence 36
                                                                                                                                                                     Example 4; SEQ ID NO 34308; 658pp + Sequence Listing;
                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                          expression in human bone marrow.
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                36 GGEEKF 41
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GGEEKF 9
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                                                                                                                                                  invention provides a number of single exon nucleic
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2000US-0234687P.
2000US-0236359P.
2000US-00024263.
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2000US-00608408.
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                                               14.6%; Score 6; 1
100.0%; Pred. No.
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Pred. No.
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                                           DB . 72;
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Matches 6
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                                               Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                    Human liver
                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                            diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the invention
                                                                                                            25-FEB-2003
                                                                                                                                     ABG55759;
                                                                                                                                                         ABG55759 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                     Sequence 36
                                                                                                                                                                                                                                                                                                                                                                            brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
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30-JUN-2000;
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Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe encoded protein SEQ ID
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nes 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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2000US-0207456P.
2000US-0060840B.
2000US-00632366.
7 2000US-0234687P.
2000US-0234359P.
2000US-0204263.
                                                                                   peptide,
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                                                                                   SEQ ID No 34407.
                                                                                                                                                                                                                                                                     14.6%; Score 6; DB
100.0%; Pred. No. 72
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                DB 4;
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                                                       Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hypaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipodaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                           Homo sapiens.
                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                              ABG43897 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000;
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2000US-0234687P.
2000US-0236359P.
2000US-00024263.
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30-JAN-2001; 2001WO-US000665

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CC complements or the 1238 open reading frames derived from the 1284 (complements or the 1284) open reading frames derived from the 1284 (c) the novel set of probes which hybridise at high stringency to a nucleic caid expressed in the human lung; measuring gene expression in a sample (c) derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung (a) array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably (c) labeled nucleic acids from eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably (c) labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, and the above mentioned microarray; assigning exons to a single exon probe (c) labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, (c) having a fragment identical to the predicted exon, the probe is included in the above and (b) measuring the expression of each of the exons in several (c) tissues and/or cell types using hybridisation to a single exon probe (c) comprising (a) identifying exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one (c) recession of the exons in the tissues and/or cell types indicates that (c) the exons should be assigned to a single gene; a peptide comprising one (c) recession of the study of lung disease (CDD), interstitial lung derived mRNA and for the study of lung disease (CDD), interstitial lung (c) lung derived mRNA and for the study of lung disease (CDD), interstitial lung (c) the invention. Nute: The sequence is a peptide comprising one (c) pulmonary haemosiderosis, pulmonary (c) pulmon
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their
                                                                                                                                   Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 33562; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spatially-addressable set of single exon nucleic acid probes, used to
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h Simi 7;	A;Status: preliminary A;Residues: 1-98 <tom; 1-98="" <tom;="" a;coss-references:="" a;residues:="" c;keywords:="" c;superfamily:="" domain:="" em="" f;15-98="" heterocetr="" immuno<="" immunog="" td=""><td></td><td></td><td></td><td>14.</td><td></td><td>14.</td><td>6 14.6</td><td>14.</td><td>14.</td><td>14.</td><td>14.</td><td>14.</td><td>14.</td><td>14.</td><td>14.</td><td>6 14.6</td></tom;>				14.		14.	6 14.6	14.	14.	14.	14.	14.	14.	14.	14.	6 14.6
17.1%; larity 100.0%; Conservative (	/ MbL:Z12304 SMBL:	Walter, G.; M. 776-798, 1992 Oire of human S26885; MUID	lon (DP-2) ens (man) eequence_r		523		461	457	436	430	416	409	401	398	398	389	375
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DB 2; Length 98; 1.8; hes 0; Indels	A;Status: preliminary A;Molecule type: DNA A;Residuse; 1-98 <tom> A;Residuse: 1-98 <tom> A;Residuse: 1-98 <tom> A;Coss-references: EMBL:Z12304; NID:g32863; PIDN:CAA78174.1; PID:g32864 A;Cross-references: EMBL:Z12304; NID:g32863; PIDN:CAA78174.1; PID:g32864 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <imm></imm></tom></tom></tom>	· · ·	gion (DP-2) - human (fragment) iens (man) #sequence_revision 10-Nov-1995 #text_change	ις.													
s ; 0;	1; PID:g3280 blogy	cer, G. s about	lange 21-Jan-2000		linoleoyl-CoA desa	hypothetical prote	sugar transferase	hypothetical prote	adenylosuccinate	two component resp	probable C3HC4 zin	probable 2,3-bispn	hypothetical prote	hypothetical	conserved hypothet	hypothetical prote	fetuin precursor
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Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor, Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69280 A;Cross-references: UNIPROT:029993; GB:AE001089; GB:AE000782; NID:92689412; PIDN:AAB9098-C;Superfamily: ferrous iron transport protein B; translation elongation factor Tu homolog C;Keywords: GTP binding; nucleotide binding; P-loop F;21-28/Region: nucleotide-binding motif A (P-loop) A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-639 <KLE> R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. iron (II) transporter (feoB-1) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004 C;Accession: F69280 Query Match N 17.1%; Score 7; DB 1; Length 639; K.A.; Dodson irkness, E.F.

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RESULT 5
ERAD74
early E3B 15.3K protein - C;Species: Mastadenovirus
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tille: Sequence and analysis of chromosome of the plant Arabidopsis.
A;Reference, number: A86141; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:P33103; EMBL:X17524; NID:g44425;
C;Superfamily: Escherichia coli ribosomal protein L24
                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Ohama, T.; P
J. Mol. Evol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein L24 - Micrococcus luteus
C;Species: Micrococcus luteus, Micrococcus lysodeikticus
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text
C;Accession: S29883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown protein, 88255-88575 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chang
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A;Residues: 1-106 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                   T.; Muto, A.; Usa:
Evol. 29, 381-395,
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381-395, 1989
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100.0%; Pr/
170 0;
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100.0%; F.
    human adenovirus
h7 (human adenovi
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100.0%; Pred. No. 25;
cive 0; Mismatches
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mismatches
      adenovirus
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                  A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                        glucosyltransferase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: AG2091
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AG2091
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                                                                                                                                                                           Nakazaki, N.; Shimpo, S.;
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
                                                                                                                                                                                                                  R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, i
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
                                         A;Cross-references: UNIPROT:Q8YUP9; GB:BA000019; PIDN:BAB73985.1; PID:g17131378; GSPDB:G
A;Experimental source: strain PCC 7120
                                                                                                                                      A; Reference number: AB1807; A; Accession: AG2091
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                                                                            A; Molecule type: DNA
A; Residues: 1-169 < KUR>
                                                                                                                     A;Status: preliminary
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  al12286
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Sequence of the Filamentous Nitrogen-fixing 7; MUID:21595285; PMID:11759840

S.; Watanabe, , M.; Yasuda,

M.; Tabata, **P** 

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Iriguchi

Cyanobacterium

Anak

strain PCC 7120 09-Jul-2004

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A;Gene: aq_yo,
C;Superfamily: Pyrococcus
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G;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C;Accession: E31830
R;Hong, J.S.; Mullis, K.G.; Engler, J.A.
Virology 167, 545-553, 1988
A;Title: Characterization of the early region 3 and fiber genes
A;Reference number: A94386; MUID:89073758; PMID:2849239
A;Accession: E31830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-135 <HON>
A;Cross-references: UNIPROT:P15135;
C;Superfamily: adenovirus early E3B
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein aq_987 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: E70385
                                                                                                                                                                                         A;Cross-references: UNIPROT:067112; GB:AE000717; NID:g2983492; PIDN:AAC07079.1; PID:g298:
A;Experimental source: strain VF5
                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-165 <AQF>
                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                   Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                     R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                              The complete genome of the hyperthermophilic bacterium Aquifex aeolicus Reference number: A70300; MUID:98196666; PMID:9537320
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Best Local |
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M. ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1538
                                                                                                                                                                                                                                                                                                                 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: AE1538
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Ar
.; Dominguez Bernal, G.; Duchaud, E.; Durand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription regulator TetR/AcrR family homolog lin0845 [imported] - Listeria C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-204 <STO>
A; Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Date: 20-Ap
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein CC0375 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Datc: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Datc: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                           A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87295
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100.0%; Pr
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Dussurget, O.; Entian, K.D.; I
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RESULT

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A;Cross-references: UNIPROT:Q8ZFQ8; C;Genetics:
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A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, A; Authors: Kreft, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. ok, C.; Schlueter, T.; Simoes, D.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1173
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AG1173
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001
C;Accession: AF0199
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog. A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: A87990
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C;Accession:
                                                                                                                                                                    protein W05H12.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change
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A; Residues: 1-216 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein lmo0791 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes (C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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A; Residues: 1-207 < KUR>
                                                                                                       R; anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                               RESULT 12
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45;
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; Entian, K.D.;
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Voss, H.; Wehland,
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Fsihi, H.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <STO>
A;Cross-references: UNIPROT:062394; GB:chr_I; PIDN:CAB04920.1; PID:g3880544; GSPDB:GN000
Query Match
Best Local Similarity
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   moeB/thiF family protein Cj0294 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; A; M.; C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1530
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                                                                                                                                                                                                                                                                   A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81448
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\;Cross-references: UNIPROT:Q92DM9; GB:AL592022; PIDN:CAC96016.1; PID:g16413235; GSPDB:
\;Experimental source: strain Clip11262
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;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend,
;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.;
                                                                                                                                                   Experimental source:
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;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                 Cross-references: UNIPROT:Q9PIK5; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB727 Experimental source: serotype O2, strain NCTC 11168
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Dussurget, O.; Entian, K.D.; I
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens)
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                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-221 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Title: The genome sequence of the facul;Reference number: AD3252; PMID:11756688
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